

SEARCH REQUEST FORM

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Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>D. Schupfer</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>272-2526</u>	AA Sequence (#) <u>2</u>	Dialog _____
Searcher Location: <u>Remsen EOI AGI</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr. Link _____
Date Completed: <u>5/28/04</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>1.2</u>	Fulltext _____	Sequence Systems <u>Compugen CCG</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Fee: <u>27</u>	Other _____	Other (specify) _____

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OM protein - protein search, using sw model

Run on: May 26, 2004, 09:24:28 ; Search time 18 Seconds
(without alignments)
1232.327 Million cell updates/sec

Title: US-09-966-781A-1

Perfect score: 2243

Sequence: 1 DQTAHYIRMLGDVVRSGAG.....DTDAAFELNSQLLPQENRLS 426

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2243	100.0	482	1 CN7A_HUMAN	Q13946 homo sapien
2	2116	94.3	426	1 CN7A_RAT	O08593 rattus norv
3	2105	93.8	456	1 CN7A_MOUSE	P70453 mus musculu
4	1403.5	62.6	450	1 CN7B_HUMAN	Q9up56 homo sapien
5	1391.5	62.0	446	1 CN7B_MOUSE	O9qxd1 mus musculu
6	555	24.7	844	1 CN4A_RAT	P54748 rattus norv
7	551	24.6	844	1 CN4A_MOUSE	O89084 mus musculu
8	550	24.5	721	1 CN4B_RAT	P14646 rattus norv
9	550	24.5	736	1 CN4B_HUMAN	Q07343 homo sapien
10	545	24.3	712	1 CN4C_HUMAN	Q08493 homo sapien
11	542	24.2	809	1 CN4D_HUMAN	Q08499 homo sapien
12	541	24.1	886	1 CN4A_HUMAN	P27815 homo sapien
13	539	24.0	672	1 CN4D_RAT	P14270 rattus norv
14	534.5	23.8	536	1 CN4C_RAT	P14644 rattus norv
15	503	22.4	829	1 CN8A_HUMAN	O60658 homo sapien
16	498.5	22.2	823	1 CN8A_MOUSE	O88502 mus musculu
17	493.5	22.0	549	1 YST1_CABEL	Q22000 caenorhabdi
18	482	21.5	664	1 YGK_CABEL	O18696 caenorhabdi
19	478.5	21.3	777	1 CNAL_DROME	P12552 drosophila
20	471.5	21.0	793	1 REGA_DICDI	Q23917 dictyosteli
21	471.5	21.0	885	1 CN8B_HUMAN	O95263 homo sapien
22	470.5	21.0	534	1 CN1B_BOVIN	Q01061 bos taurus
23	470.5	21.0	535	1 CN1B_MOUSE	O01065 mus musculu
24	469.5	20.9	535	1 CN1B_RAT	Q01066 rattus norv
25	466	20.8	654	1 CN1C_MOUSE	Q64338 mus musculu
26	461	20.6	768	1 CN1C_RAT	Q63421 rattus norv
27	457.5	20.4	536	1 CN1A_HUMAN	Q01064 homo sapien
28	456.5	20.4	565	1 CN1A_MOUSE	Q61481 mus musculu
29	452	20.2	534	1 CN1A_HUMAN	P54750 homo sapien
30	452	20.2	709	1 CN1C_HUMAN	Q14123 homo sapien
31	439.5	19.6	529	1 CN1A_BOVIN	P14100 bos taurus
32	418	18.6	534	1 CN9A_MOUSE	O70628 mus musculu
33	412	18.4	593	1 CN9A_HUMAN	O76083 homo sapien

ALIGNMENTS

RESULT 1

CN7A_HUMAN

ID CN7A_HUMAN STANDARD; PRT; 482 AA.

AC Q13946; Q15380;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A

DE (EC 3.1.4.17) (HCP1) (TM22).

GN PDE7A.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM PDE7A1).

RX MEDLINE=93286141; PubMed=8389765;

RA Michael T., Bloom T.J., Martins T., Loughney K., Ferguson K.,

RA Riggs M., Rodgers L., Beavo J.A., Wigler M.;

RT "Isolation and characterization of a previously undetected human cAMP

phosphodiesterase by complementation of cAMP phosphodiesterase-

RT deficient Saccharomyces cerevisiae,"

RL J. Biol. Chem. 268:12925-12932(1993).

[2]

RP SEQUENCE FROM N.A. (ISOFORM PDE7A2).

RX TISSUE=Skeletal muscle;

RC MEDLINE=97341143; PubMed=9195912;

RA Han P., Zhu X., Michael T.;

RT "Alternative splicing of the high affinity cAMP-specific

phosphodiesterase (PDE7A) mRNA in human skeletal muscle and heart.";

RL J. Biol. Chem. 272:16152-16157(1997).

CC !- FUNCTION: Plays a role in signal transduction by regulating the

intracellular concentration of cyclic nucleotides. This

phosphodiesterase is highly specific for cAMP and may have a role

in muscle signal transduction.

CC !- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =

adenosine 5'-phosphate.

CC !- COFACTOR: Requires divalent cations.

CC !- ENZYME REGULATION: Insensitive to all selective PDE inhibitors.

CC !- PATHWAY: Cyclic nucleotide metabolism.

CC !- SUBCELLULAR LOCATION: PDE7A1 (57 KDA) IS LOCATED MOSTLY TO SOLUBLE

CELLULAR FRACTIONS. PDE7A2 (50 KDA) IS LOCATED TO PARTICULATE

CELLULAR FRACTIONS.

CC !- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=PDE7A1;

Isoid=Q13946-1; Sequence=Displayed;

Name=PDE7A2;

Isoid=Q13946-2; Sequence=VSP_004593;

CC !- TISSUE SPECIFICITY: PDE7A1 is found at high levels in skeletal

muscle and at low levels in a variety of tissues including brain

and heart. It is expressed as well in two T-cell lines. PDE7A2 is

found abundantly in skeletal muscle and at low levels in heart.

CC !- DEVELOPMENTAL STAGE: Developmentally regulated. PDE7A1 and PDE7A2

are found in several fetal tissues, expression is reduced

throughout development. It persists strongly only in adult

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CC skeletal muscle.
CC -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC putative divalent metal sites and an N-terminal regulatory domain.
CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC family.
CC
CC -----
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CC -----
CC EMBL: L12052; AAA35644.2; -
CC EMBL: U67932; AAB65772.1; -
CC Genew: HGNC:8791; PDE7A.
CC MIM: 171885; -
CC GO: GO:000267; C:cell fraction; NAS.
CC GO: GO:0004115; F:CAMP-specific phosphodiesterase activity; TAS.
CC GO: GO:0007165; P:signal transduction; NAS.
CC InterPro: IPR003607; Met_phosphohydro.
CC InterPro: IPR002073; PDEase.
CC Pfam: PF00233; PDEase; 1.
CC PRINTS: PR00387; PDIESTERASE1.
CC SMART: SM00471; HDC; 1.
CC PROSITE: PS00126; PDEASE_I; 1.
CC Hydrolase; CAMP; Phosphorylation; Alternative splicing.
CC DOMAIN 28 33 POLY-SER.
CC MOD_RES 187 451 CATALYTIC (BY SIMILARITY).
CC VARSPLIC 84 84 PHOSPHORYLATION (POTENTIAL).
CC MEVCYLPVLPDRPVPQVLSRRGAISSSSSALFGCPNP
CC ROLSQ -> MGITLWCLALVLKWTISK (in isoform
CC PDE7A2).
CC /FTID-VSP 004593.
CC SEQUENCE 482 AA; 55505 MW; 3B3C8F6E9154F88C CRC64;
CC
CC Query Match 100.0%; Score 2243; DB 1; Length 482;
CC Best Local Similarity 100.0%; Pred. No. 1.4e-176;
CC Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 DQATYIRMLGDVVRSRAGFESERGGSHPYIDFRIFHSQSEIEVSARNIRLLSFQR 60
CC Db 57 DQATYIRMLGDVVRSRAGFESERGGSHPYIDFRIFHSQSEIEVSARNIRLLSFQR 116
CC QY 61 YLRSSRFRTAVSNLILDDYNGQAKCMLEKGVNWNFDIFLDRLTNGNSLVSLTFH 120
CC Db 117 YLRSSRFRTAVSNLILDDYNGQAKCMLEKGVNWNFDIFLDRLTNGNSLVSLTFH 176
CC QY 121 LFSHGLIEYFHLDMKLRRLVMIQEDYHSQNPYHNAVAADVTQAMHCYLKEPKLAN 180
CC Db 177 LFSHGLIEYFHLDMKLRRLVMIQEDYHSQNPYHNAVAADVTQAMHCYLKEPKLAN 236
CC QY 181 VTPWDILLSIAAATHDLDPGVNQPLIKTNHYLATLYKNTSVLENHHSRVAGLLRSS 240
CC Db 237 VTPWDILLSIAAATHDLDPGVNQPLIKTNHYLATLYKNTSVLENHHSRVAGLLRSS 296
CC QY 241 GLFSLHPLSRQOMETQIGALIIATDISKQNEYLSLFRSHLDRGDLCLEDTTRHVLQ 300
CC Db 297 GLFSLHPLSRQOMETQIGALIIATDISKQNEYLSLFRSHLDRGDLCLEDTTRHVLQ 356
CC QY 301 ALKADICNPCRTELKQWSEKVTETFEHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
CC Db 357 ALKADICNPCRTELKQWSEKVTETFEHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 416
CC QY 361 MTYLVEPLETWARFNTRLSQTMGLGVGLKASWGLQREQSSSEDTDAAFINSQLLP 420
CC Db 417 MTYLVEPLETWARFNTRLSQTMGLGVGLKASWGLQREQSSSEDTDAAFINSQLLP 476
CC QY 421 QENRLS 426
CC Db 477 QENRLS 482

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RESULT 2

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CNVA_RAT ID CNVA_RAT STANDARD; PRT; 426 AA.
AC 008593;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE High-affinity CAMP-specific 3',5'-cyclic phosphodiesterase 7A
DE (EC 3.1.4.17) (Rolipram-insensitive phosphodiesterase type 7)
DE (Fragment).
GN PDE7A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98176136; PubMed=9515162;
RA Hoffmann R., Abdel'Al S., Engels P.;
RT "Differential distribution of rat PDE-7 mRNA in embryonic and adult
RL Cell Biochem. Biophys. 28:103-113(1998).
CC -!- FUNCTION: Plays a role in signal transduction by regulating the
CC intracellular concentration of cyclic nucleotides. This
CC phosphodiesterase is highly specific for CAMP and may have a role
CC in muscle signal transduction (By similarity).
CC -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC adenosine 5'-phosphate.
CC -!- COFACTOR: Requires divalent cations (By similarity).
CC -!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors (By
CC similarity).
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC putative divalent metal sites and an N-terminal regulatory domain.
CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC family.
CC -----
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CC -----
CC EMBL: U77880; AAB51234.1; -
CC InterPro: IPR003607; Met_phosphohydro.
CC Pfam: PF00233; PDEase; 1.
CC PRINTS: PR00387; PDIESTERASE1.
CC SMART: SM00471; HDC; 1.
CC PROSITE: PS00126; PDEASE_I; 1.
CC Hydrolase; CAMP.
CC NON_TER 1 1
CC DOMAIN 131 395 CATALYTIC (BY SIMILARITY).
CC SEQUENCE 426 AA; 49274 MW; 129BDC01C9351D26 CRC64;
CC
CC Query Match 94.3%; Score 2116; DB 1; Length 426;
CC Best Local Similarity 94.1%; Pred. No. 3.2e-166;
CC Matches 401; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
CC
CC QY 1 DQATYIRMLGDVVRSRAGFESERGGSHPYIDFRIFHSQSEIEVSARNIRLLSFQR 60
CC Db 1 DQATYIRMLGDVVRSRAGFETERRGGSHPYIDFRIFHSQSEIEVSARNIRLLSFQR 60
CC QY 61 YLRSSRFRTAVSNLILDDYNGQAKCMLEKGVNWNFDIFLDRLTNGNSLVSLTFH 120
CC Db 61 YLRSSRFRTAVSNLILDDYNGQAKCMLEKGVNWNFDIFLDRLTNGNSLVSLTFH 120
CC QY 121 LFSHGLIEYFHLDMKLRRLVMIQEDYHSQNPYHNAVAADVTQAMHCYLKEPKLAN 480

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Db 121 LFSHGLIEYFHLDMVKLRRLVLMQEDYHSQNPYHNAHAAVDTQAMHCYKLPKANS 180
 QY 181 VTPWDILLSIAAATHDLDHPGVNPFLLKTNHYLATLYKNTSVLENHHSWAVGLRES 240
 Db 181 VTPWDILLSIAAATHDLDHPGVNPFLLKTNHYLATLYKNTSVLENHHSWAVGLRES 240
 QY 241 GLFSLHPLSRQMETOIGALILATDISRQNEYLSPFRSHLDGRDGLCIEDTRHRLVLMQ 300
 Db 241 GLFSLHPLSRQMETOIGALILATDISRQNEYLSPFRSHLDGRDGLCIEDTRHRLVLMQ 300
 QY 301 ALKCADICNCRWELSKQSEKVTSEFFHQDIEKKYHGLVSPICDRHTESIANIQGF 360
 Db 301 ALKCADICNCRWELSKQSEKVTSEFFHQDIEKKYHGLVSPICDRHTESIANIQGF 360
 QY 361 MTYLVEPLFTWARFSNTRLSQTMGLHGVNLSKWSKGLQREQSSSEDTDAFAELNSQLLP 420
 Db 361 MTYLVEPLFTWARFSNTRLSQTMGLHGVNLSKWSKGLQREQSSSEDTDAFAELNSQLLP 420
 QY 421 QENRLS 426
 Db 421 QENRLS 426

RESULT 3

CNVA_MOUSE STANDARD; PRT; 456 AA.
 AC P70453; Q9ERB3;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A
 DE (EC 3.1.4.17) (P2A).
 GN PDE7A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=97098542; PubMed=8943082;
 RA Bloom T.J., Beavo J.A.;
 RT "Identification and tissue-specific expression of PDE7
 RT phosphodiesterase splice variants.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14188-14192 (1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain, and Testis;
 RX MEDLINE=20483661; PubMed=11027622;
 RA Wang P., Wu P., Egan R.W., Billah M.M.;
 RT "Cloning, characterization, and tissue distribution of mouse
 RT phosphodiesterase 7A1.";
 RL Biochem. Biophys. Res. Commun. 276:1271-1277 (2000).
 CC -!- FUNCTION: Plays a role in signal transduction by regulating the
 CC intracellular concentration of cyclic nucleotides. This
 CC phosphodiesterase is highly specific for cAMP and may have a role
 CC in muscle signal transduction.
 CC -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
 CC adenosine 5'-phosphate.
 CC -!- COFACTOR: Requires divalent cations.
 CC -!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors.
 CC -!- PATHWAY: Cyclic nucleotide metabolism.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1; Synonyms=PDE7A2;
 CC IsoId=P70453-1; Sequence=Displayed;
 CC Name=2; Synonyms=PDE7A1;
 CC IsoId=P70453-2; Sequence=VSP_004594;
 CC -!- TISSUE SPECIFICITY: Widely expressed with highest levels in the
 CC skeletal muscle.
 CC -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
 CC putative divalent metal sites and an N-terminal regulatory domain.

CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
 CC family.
 CC
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 CC
 CC EMBL; U68171; AAB08479.1; -;
 CC EMBL; AY007702; AAG16295.1; -;
 CC MGD; MGI:1202402; Pde7a.
 CC InterPro; IPR003607; Met_phosphohydro.
 CC InterPro; IPR002073; PDEase.
 CC Pfam; PF00233; PDEase; 1.
 CC PRINTS; PR00387; PDIESTERASE1.
 CC SMART; SM00471; HDC; 1.
 CC PROSITE; PS00126; PDEASE_I; 1.
 CC Hydrolase; cAMP; Alternative splicing.
 CC DOMAIN 161 425
 CC VARSPLIC 1 20
 CC QHVLRRGALSFSSSSALFCGPRQLSQ (in isoform
 CC 2).
 CC /FTId=VSP_004594.
 CC CONFLICT 407 407
 CC SEQUENCE 456 AA; 52441 MW; 0B826B96490D9F6E CRC64;
 CC
 CC Query Match 93.8%; Score 2105; DB 1; Length 456;
 CC Best Local Similarity 93.7%; Pred. No. 2.8e-165;
 CC Matches 399; Conservative 13; Mismatches 14; Indels 0; Gaps 0;
 CC
 CC QY 1 DOTALYIRMLGDVVRVSRAFGESRSGHPYIDFRIFHSQSEIEVSARNIRLLSFQR 60
 CC Db 31 DOTALYIRMLGDVVRVSRAFGESRSGHPYIDFRIFHSQSEIEVSARNIRLLSFQR 90
 CC
 CC QY 61 YLRSSRFPGTAVNSLNLDDDDYNGQAKCMLEKGVNWNFDIFLFDRLTNGSLVSLTFH 120
 CC Db 91 YLRSSRFPGTAVNSLNLDDDDYNGQAKCMLEKGVNWNFDIFLFDRLTNGSLVSLTFH 150
 CC
 CC QY 121 LFSHGLIEYFHLDMVKLRRLVLMQEDYHSQNPYHNAHAAVDTQAMHCYKLPKANS 180
 CC Db 151 LFSHGLIEYFHLDMVKLRRLVLMQEDYHSQNPYHNAHAAVDTQAMHCYKLPKANS 210
 CC
 CC QY 181 VTPWDILLSIAAATHDLDHPGVNPFLLKTNHYLATLYKNTSVLENHHSWAVGLRES 240
 CC Db 211 VTPWDILLSIAAATHDLDHPGVNPFLLKTNHYLATLYKNTSVLENHHSWAVGLRES 270
 CC
 CC QY 241 GLFSLHPLSRQMETOIGALILATDISRQNEYLSPFRSHLDGRDGLCIEDTRHRLVLMQ 300
 CC Db 271 GLFSLHPLSRQMETOIGALILATDISRQNEYLSPFRSHLDGRDGLCIEDTRHRLVLMQ 330
 CC
 CC QY 301 ALKCADICNCRWELSKQSEKVTSEFFHQDIEKKYHGLVSPICDRHTESIANIQGF 360
 CC Db 331 ALKCADICNCRWELSKQSEKVTSEFFHQDIEKKYHGLVSPICDRHTESIANIQGF 390
 CC
 CC QY 361 MTYLVEPLFTWARFSNTRLSQTMGLHGVNLSKWSKGLQREQSSSEDTDAFAELNSQLLP 420
 CC Db 391 MTYLVEPLFTWARFSNTRLSQTMGLHGVNLSKWSKGLQREQSSSEDTDAFAELNSQLLP 450
 CC
 CC QY 421 QENRLS 426
 CC Db 451 QENRLS 456
 CC
 CC RESULT 4
 CC CNVB_HUMAN STANDARD; PRT; 450 AA.
 CC ID CNVB_HUMAN
 CC AC Q9NP56;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
 GN PDE7B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20275458; PubMed=10814504;
 RA Sasaki T., Kotera J., Yuasa K., Omori K.;
 RT "Identification of human PDE7B, a CAMP-specific phosphodiesterase";
 RL Biochem. Biophys. Res. Commun. 271:575-583(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=20329226; PubMed=10872825;
 RA Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
 RT "Cloning and characterization of the human and mouse PDE7B, a novel
 CAMP-specific nucleotide phosphodiesterase";
 RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
 CC -!- FUNCTION: May be involved in the control of cAMP-mediated neural
 activity and cAMP metabolism in the brain.
 CC -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
 adenosine 5'-phosphate.
 CC -!- COFACTOR: Requires divalent cations (By similarity).
 CC -!- ENZYME REGULATION: Inhibited by dipyrindamole, IBMX and SCH51866.
 CC -!- INSENSITIVE TO zaprinast, rolipram, and milrinone.
 CC -!- PATHWAY: Cyclic nucleotide metabolism.
 CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Also expressed in
 heart, liver, skeletal muscle and pancreas.
 CC -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
 putative divalent metal sites and an N-terminal regulatory domain.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
 family.
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 CC
 CC EMBL; AB038040; BAB96537.1; -;
 CC EMBL; AJ251860; CAB92441.1; -;
 CC PIR; JC7266; JC7266.
 CC PDB; 1LXW; 26-JUN-02.
 CC Genew; HGNC:8792; PDE7B.
 CC MIM; 604645; -;
 CC GO; GO:0004115; F:CAMP-specific phosphodiesterase activity; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC GO; GO:0007268; P:synaptic transmission; TAS.
 CC InterPro; IPR003607; Met_phosphohydro.
 CC Pfam; PF002073; PDEase.
 CC Pfam; PF00233; PDEase; 1.
 CC PRINTS; PR00387; PDIESTERASE1.
 CC SMART; SM00471; Hdc; 1.
 CC PROSITE; PS00126; PDEASE_I; 1.
 CC KEGG; K04402; PDEASE_I; 1.
 CC HYDROLASE; CAMP; 3D-structure.
 CC FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).
 CC SEQUENCE 450 AA; 51835 MW; EC142BF3E28D0028 CRC64;
 CC
 CC Query Match 62.6%; Score 1403.5; DB 1; Length 450;
 CC Best Local Similarity 62.6%; Pred. No. 1e-107;
 CC Matches 258; Conservative 66; Mismatches 87; Indels 1; Gaps 1;
 CC
 CC 1 DOTALYRLMGDVVRSGFESRSHYDIFRPHSQSEVSVARNIRLLSFQR 60
 CC 18 DQAKVCVLMGDLIRLQTVARRRGSYPFDRLNLTSTYSGEIGTKKKVRLLSFQR 77
 CC
 CC 61 YLRSSRRFRGTAVSNSINILDDYNGQAKCMLEKVGNNWDFIDRLTNGNSLVSTF 120
 CC
 CC

78 YFASRLARGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFIDFLDRLTNGNSLVLLCH 137
 QY 121 LPSLHGLIEYFHLDMMLRRFLVMIQEDYHSQPNYHNAVHADVTQAMECYLKEPKLANS 180
 DB 138 LFNTHGLIHHFKLDWVTLHRLFLVMVQEDYHSQPNYHNAVHADVTQAMECYLKEPKLASF 197
 QY 181 VTPWDILLSLTAATHDLDHGVNQPFLLIKNNHYLATLYKNTSVLENHHWSAVGLRES 240
 DB 198 LTFPDLIMGLLAAAHADVDPGVNQPFLLIKNNHLNLYQNMVLENHHWSTIGMLRES 257
 QY 241 GLFSLPLESRQQMETQIGALILATDISKQNEYLSLFSLHLDGDLCLDTEHRLHVLQ 300
 DB 258 RLLAHLPEKMTQDIEQLGSLILATDINRQNEFLRLKAHLNKLRLDQDRHFMQI 317
 QY 301 ALKCADI CNPRTWELSKQWSEKTEFFHQDIEKKYHLGVSPICDRHTESIANIQIGF 360
 DB 318 ALKCADI CNPRTWELSKQWSEKTEFFHQDIEKKYHLGVSPICDRHTESIANIQIGF 377
 QY 361 MTLVPEPLFTWARFS-NTRLISQTMGLHGVNKLKASWKLQREQSSEDTDA 411
 DB 378 MSYIPEPLFREWAHFTGNSTLSENMLGHLAHLNKAQWKSLLPRQHRSGSGS 429
 RESULT 5
 CN7B_MOUSE
 ID CN7B_MOUSE STANDARD; PRT; 446 AA.
 AC Q9OXQ1.
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
 GN PDE7B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20087273; PubMed=10618442;
 RA Hetman J.M., Soderling S.H., Glavas N.A., Beavo J.A.;
 RT "Cloning and characterization of PDE7B, a CAMP-specific
 phosphodiesterase";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:472-476(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20329226; PubMed=10872825;
 RA Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
 RT "Cloning and characterization of the human and mouse PDE7B, a novel
 CAMP-specific nucleotide phosphodiesterase";
 RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
 CC -!- FUNCTION: May be involved in the control of cAMP-mediated neural
 activity and cAMP metabolism in the brain.
 CC -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
 adenosine 5'-phosphate.
 CC -!- COFACTOR: Requires divalent cations (By similarity).
 CC -!- ENZYME REGULATION: Inhibited by dipyrindamole, IBMX and SCH51866.
 CC -!- INSENSITIVE TO zaprinast, rolipram, and milrinone.
 CC -!- PATHWAY: Cyclic nucleotide metabolism.
 CC -!- TISSUE SPECIFICITY: Highly expressed in brain.
 CC -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
 putative divalent metal sites and an N-terminal regulatory domain.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
 family.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC

"Differential CNS expression of alternative mRNA isoforms of the mammalian genes encoding cAMP-specific phosphodiesterases."; Gene 149:237-244 (1994).

[3]

RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=86132847; PubMed=8557632;
RA Bolger G.B., McPhee I., Houslay M.D.;
RT "Alternative splicing of cAMP-specific phosphodiesterase mRNA transcripts. Characterization of a novel tissue-specific isoform, RNPDE4A8.";
RL J. Biol. Chem. 271:1065-1071(1996).

[4]

RP SEQUENCE OF 319-677 FROM N.A. (ISOFORM 3/4).
RC TISSUE=Testis;
RX MEDLINE=893115790; PubMed=2546153;
RA Swinnen J.V., Joseph D.R., Conti M.;
RT "Molecular cloning of rat homologues of the Drosophila melanogaster cAMP phosphodiesterase: evidence for a family of genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329(1989).

[5]

RP STRUCTURE BY NMR OF 1-26 OF ISOFORM 3.
RX MEDLINE=96279244; PubMed=8663181;
RA Smith K.J., Scotland G., Beattie J., Trayer I.P., Houslay M.D.;
RT "Determination of the structure of the N-terminal splice region of the cyclic AMP-specific phosphodiesterase RDL (RNPDE4A1) by 1H NMR and identification of the membrane association domain using chimeric constructs.";
RL J. Biol. Chem. 271:16703-16711(1996).

[6]

CC -1- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O -> adenosine 5'-phosphate.
CC -1- ENZYME REGULATION: Inhibited by rolipram.
CC -1- PATHWAY: Cyclic nucleotide metabolism.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Name=1;
CC IsoId=P54748-1; Sequence=Displayed;
CC Name=2; Synonyms=PDE4A8;
CC IsoId=P54748-2; Sequence=VSP_004565;
CC Name=3;
CC IsoId=P54748-3; Sequence=VSP_004566, VSP_004567;
CC Name=4; Synonyms=Medium;
CC IsoId=P54748-4; Sequence=VSP_004568;
CC Name=5; Synonyms=Short;
CC IsoId=P54748-5; Sequence=VSP_004569, VSP_004570;
CC -1- TISSUE SPECIFICITY: Isoform 2 is testis specific.
CC -1- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterases family.

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CC EMBL; L27057; AAC27098.1; -
CC EMBL; L36467; AAB00357.1; -
CC EMBL; L27062; AAA56859.1; -
CC EMBL; M25348; AAA41848.1; -
CC EMBL; M28411; AAA41823.1; -
CC EMBL; M26715; AAC37699.1; -
CC EMBL; M26716; AAA41691.1; -
CC EMBL; M26717; AAA41102.1; -
CC PIR; I53865; I53865.
CC PIR; I67946; I67946.
CC PDB; 1LOI; 15-MAY-97.
CC InterPro; IPR003607; Met_phosphohydro.
CC InterPro; IPR002073; PDEase.
CC Pfam; PF00233; PDEase; 1.
CC PRINTS; PR00387; PDIESTERASE1.
CC SMART; SM00471; HDC; 1.

Olsen A.E., Bolger G.B.;
"Physical mapping and promoter structure of the murine cAMP-specific
phosphodiesterase pde4a gene."; *Mamm. Genome* 11:41-45(2000).
[2]
SEQUENCE FROM N.A. (ISOFORM 2), AND ENZYME REGULATION.
RT TISSUE=Brain;
RP MEDLINE=21167369; PubMed=11267656;
RX Cherry J.A., Thompson B.E., Pho V.;
"Diazepam and rolipram differentially inhibit cyclic AMP-specific
phosphodiesterases PDE4A1 and PDE4B3 in the mouse."; *Biochim. Biophys. Acta* 1518:27-35(2001).
[3]
SEQUENCE FROM N.A. (ISOFORM 3).
RT TISSUE=Salivary gland;
RP MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Rahra S.S., Loquellano N.A., Toshiyuki S., Carninci P., Prange C.,
Bosak S.A., McSwan P.J., Peters G.J., Abramson R.D., Mullan S.J.,
Richards S., Worley K.J., McKernan K.J., Walek J.A., Gunaratne P.H.,
Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."; *Proc. Natl. Acad. Sci. U.S.A.* 99:16899-16903(2002).
[4]
SEQUENCE OF 248-355 FROM N.A. (ISOFORM 2).
RT TISSUE=Brain;
RP MEDLINE=98343959; PubMed=9677330;
RX Sullivan M., Rana G., Begg F., Gordon L., Olsen A.S., Houslay M.D.;
"Identification and characterization of the human homologue of the
short PDE4A cAMP-specific phosphodiesterase 4A variant RD1 (PDE4A1)
analysis of the human HSPDE4A gene locus located at chromosome
19p13.2."; *Biochem. J.* 333:693-703(1998).
RL -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC adenosine 5'-phosphate
CC -!- ENZYME REGULATION: Inhibited by rolipram and diazepam.
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=O89084-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O89084-2; Sequence=VSP_004563, VSP_004564;
CC Name=3;
CC IsoId=O89084-3; Sequence=VSP_004562;
CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF142646; AAF14519.1; -
DR EMBL; AF142643; AAF14519.1; JOINED.
DR EMBL; AF142644; AAF14519.1; JOINED.

GN PDE4B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM PDE4B3).
 RA Huston E., Simon L., Annette R., Catterall C., Ross A.H., Steele M.R.,
 RA Bolger G.B., Perry M., Owens R., Houslay M.D.;
 RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE OF 160-721 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=89264471; PubMed=2542941;
 RA Colicelli J., Birchmeier C., Michaeli T., O'Neill K., Riggs M.,
 RA Wigler M.;
 RL "Isolation and characterization of a mammalian gene encoding a high-
 affinity cAMP phosphodiesterase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:3599-3603 (1989).
 RP [3]
 RP SEQUENCE OF 289-638 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=89315790; PubMed=2546153;
 RA Swinnen J.V., Joseph D.R., Conti M.;
 RL "Molecular cloning of rat homologues of the Drosophila melanogaster
 dunce cAMP phosphodiesterase: evidence for a family of genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329 (1989).
 RP [4]
 RP SEQUENCE FROM N.A. (ISOFORM PDE4B2).
 RX MEDLINE=95047482; PubMed=7958996;
 RA Bolger G.B., Rodgers L., Riggs M.;
 RL "Differential CNS expression of alternative mRNA isoforms of the
 mammalian genes encoding cAMP-specific phosphodiesterases.";
 RL Gene 149:237-244 (1994).
 RP [5]
 RP SEQUENCE FROM N.A. (ISOFORM PDE4B2).
 RC STRAIN=Wistar;
 RX MEDLINE=94103234; PubMed=8276818;
 RA Monaco L., Vicini E., Conti M.;
 RL "Structure of two rat genes coding for closely related rolipram-
 sensitive cAMP phosphodiesterases. Multiple mRNA variants originate
 from alternative splicing and multiple start sites.";
 RL J. Biol. Chem. 269:347-357 (1994).
 CC -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
 CC adenosine 5'-phosphate.
 CC -!- ENZYME REGULATION: Inhibited by rolipram.
 CC -!- PATHWAY: Cyclic nucleotide metabolism.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=3;
 CC Comment=Additional isoforms seem to exist;
 CC Name=PDE4B3;
 CC IsoId=PI4646-1; Sequence=Displayed;
 CC Name=PDE4B1;
 CC IsoId=PI4646-3; Sequence=Not described;
 CC Name=PDE4B2;
 CC IsoId=PI4646-2; Sequence=VSP_004573;
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
 CC family.
 CC
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 CC
 CC EMBL; U95748; AAB96560.1; -;
 CC EMBL; J04563; AAB6039.1; -;
 CC EMBL; M25350; AAA41846.1; -;
 CC EMBL; M28413; AAA41824.1; -;
 CC EMBL; L27058; AAA74478.1; -;
 CC EMBL; U01291; AAA18926.1; -;
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 CC DR EMBL; M25350; AAA41846.1; -;
 CC DR EMBL; M28413; AAA41824.1; -;
 CC DR EMBL; L27058; AAA74478.1; -;
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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DR EMBL; AF157814; AAD47054.1; JOINED.
DR EMBL; AF157815; AAD47054.1; JOINED.
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DR EMBL; AF157815; AAD47055.1; JOINED.
DR EMBL; AC005759; AAC83047.1; -.
DR EMBL; L20368; AAA03591.1; -.
DR PIR; S71626; S71626.
DR PDB; 1LXU; 26-JUN-02.
DR Genew; HGNC:8782; PDE4C.
DR MIM; 600128; -.
DR GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
DR InterPro; IPR003607; Met phosphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00367; PDESTERASE1.
DR SMART; SMO0471; Hdc; 1.
DR PROSITE; PS00126; PDEASE 1; 1.
DR KEGG; K04471; Hdc; 1.
DR KW; Hydrolase; cAMP; Multigene family; Alternative splicing; 3D-structure.
DR FT; VARSPLIC 1 81
MENLGVGGAACACSELSRSGHSMTRAPKHLWQPRPRIR
IQQREYSPDPSKAGCERDLSPRLKSLRSLWPSVSCRR
--> MGGPAPAPVPVPGSPGSPGSLFKLLVNSGIRL
QRRTVAHPLC (in isoform PDE4C3).
/FTid=VSP_004574.
Missing (in isoform PDE4C2).
/FTid=VSP_004575.
K -> N (IN REF. 2).
D -> Y (IN REF. 2).
EL -> DV (IN REF. 1).
NSE -> K (IN REF. 3).
EL -> DV (IN REF. 1).
EL -> DV (IN REF. 1).
SQ SEQUENCE 712 AA; 79901 MW; 1932116C9CE0322C CRC64;

Query Match 24.3%; Score 545; DB 1; Length 712;
Best Local Similarity 33.8%; Pred. No. 5.6e-37;
Matches 125; Conservative 68; Mismatches 153; Indels 24; Gaps 7;

QY 22 ESRRGGH--PYIDRFIFHSQSEIEV-SVSARNIRRLLSFORYLRSRFFRGTAVSLSLN 78
Db 250 ETSRSGNOVSYSISRTFLDQTEVELPKVTAABAPQMS-----RISG-LHGLCHSASLS 303
QY 79 I-----LDDYNGQAKMCLKVGNMNFIDFLDRLTNGSLVSLTFLHLSHLGLIEYF 131
Db 304 SATVPRFGVQTDQEQLEAKLEDITKMGDLVFKVAELSGNRPFLTAIFSIQERDLKTF 363
QY 132 HLDMMKLRRLFLVLMQEDVHSQNPYHNAHADVTQAMHCYIKPKLANSVTFPMDILSLI 191
Db 364 QIPADTTLATYLLMLLEGHYHANVYHNSLHAADVAQSTHVLATPALEAVFTDLLEALF 423
QY 192 AAATHDLDPGVNQPFLIKTHYLATLYKNTSVLENHHWSAVGLLRBSG--LFSHLPLE 249
Db 424 ASALHVDVHPGVSNQFLINTSELALMYNDASVLENHHLAVGFKLLQAENCDIFQNLAK 483
QY 250 SRQOMETQIGALIIATDISRQNEYSLSFRSHLDR-----GDLCLETRHRLHVLQWALK 303
Db 484 QRLSLRRLVMDVLATDMSKHMNLADLKVTETKVTSLGVLDDVSDRIQVLQNLVH 543
QY 304 CADICNPCTWELSKQSEKYTEFFHGDTLEKKYHLGVSPICDRHTESIANIQIGWY 363
Db 544 CADLSNPKPLPLRYQWTDRIAMAFQFQGGDRERSGLDISPMCDKHTASVEKSVQGFIDY 603
QY 364 LVEPLFTWA 373
Db 604 IAHPLMETWA 613

RESULT 11
CN4D HUMAN
ID -CN4D HUMAN STANDARD; PRT; 809 AA.
AC Q08499; Q08433; Q13549; Q13550; Q13551;
DT 01-OCT-1996 (Rel. 34, Created)

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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE CAMP-specific 3',5'-cyclic phosphodiesterase 4D (BC 3.1.4.17)
DE (PDE3) (PDE43).
DE GN PDE4D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=94019330; PubMed=8413254;
RA Bolger G.B., Michaeli T., Martins T., John T., Steiner B.,
RA Rodgers L., Biggs M., Wigler M., Ferguson K.;
RT "A family of human phosphodiesterases homologous to the duncce
RT learning and memory gene product of Drosophila melanogaster are
RT potential targets for antidepressant drugs.";
RL Mol. Cell. Biol. 13:6558-6571(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6), AND REVISIONS TO
RP ISOFORM 1.
RX MEDLINE=98041897; PubMed=9371713;
RA Bolger G.B., Erdogan S., Jones R.E., Loughney K., Scotland G.,
RA Hofmann R., Wilkinson I., Farrell C., Houslay M.D.;
RT "Characterization of five different proteins produced by
RT alternatively spliced mRNAs from the human cAMP-specific
RT phosphodiesterase PDE4D gene.";
RL Biochem. J. 328:539-548(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX TISSUE=Heart;
RA MEDLINE=94171048; PubMed=8125310;
RA Baekker P.A., Oberholte R., Bach C., Yee C., Shelton E.R.;
RT "Isolation of a cDNA encoding a human rolipram-sensitive cyclic AMP
RT phosphodiesterase (PDE IVD).";
RL Gene 138:253-256(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 4 AND 5).
RX MEDLINE=96390839; PubMed=8797812;
RA Nemcz G., Zhang R.B., Sette C., Conti M.;
RT "Identification of cyclic AMP-phosphodiesterase variants from the
RT PDE4D gene expressed in human peripheral mononuclear cells.";
RL FEBS Lett. 384:97-102(1996).
CC -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC adenosine 5'-phosphate.
CC -!- ENZYME REGULATION: Inhibited by rolipram.
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Name=1; Synonyms=hpDE4D4;
CC IsoId=Q08499-1; Sequence=Displayed;
CC Name=2; Synonyms=hpDE4D3;
CC IsoId=Q08499-2; Sequence=VSP_004577;
CC Name=3;
CC IsoId=Q08499-3; Sequence=VSP_004578;
CC Name=4; Synonyms=hpDE4D1;
CC IsoId=Q08499-4; Sequence=VSP_004579;
CC Name=5; Synonyms=hpDE4D2;
CC IsoId=Q08499-5; Sequence=VSP_004580;
CC Name=6; Synonyms=hpDE4D5;
CC IsoId=Q08499-6; Sequence=VSP_004576;
CC -!- TISSUE SPECIFICITY: WIDESPREAD; MOST ABUNDANT IN SKELETAL MUSCLE.
CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC family.
CC
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DR	EMBL; U69532; AAC3832.1; --.
DR	EMBL; U97584; AAC25679.1; --.
DR	EMBL; BC019864; AAH19864.1; --.
DR	PIR; A54442; A54442.
DR	PIR; S55348; S55348.
DR	Genew; HGNC:8780; PDE4A.
DR	MIM; 600126; --.
DR	GO; GO:0005626; C:insoluble fraction; TAS.
DR	GO; GO:0005624; C:membrane fraction; TAS.
DR	GO; GO:0005625; C:soluble fraction; TAS.
DR	GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
DR	GO; GO:0007165; P:signal transduction; TAS.
DR	InterPro; IPR003607; Met_phosphohydro.
DR	InterPro; IPR002073; PDEase.
DR	Pfam; PF00233; PDease; 1.
DR	PRINTS; PR00387; PDIESTERASE1.
DR	SMART; SM00471; HDG; 1.
DR	PROSITE; PS00126; PDEASE_I; 1.
KW	Hydrolase; cAMP; Alternative
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FT	MEPTVPSERSLSLSLPFGREGATLKPPQHLWRQPRTPI
FT	RIOQRGYSDSAERAERQPHRIERADAMDTSDRPLGRIT
FT	RMWPSPFHGTGTGGAGGSSRRFEANGPTTSPGRSPL
FT	DSQAQGLVLHAGAATSORRESFLYSDSDYDMSPKTMSRN
FT	SVVTSABAHDLIVTPFAQVLASLRSVRNSFSLLTNVVPVS
FT	NKESPLGGPVPCKATLSEETCOQLARETELELDWCLEOLE
FT	TMTYISVSEMASHK -> MPLVDFFCETCSKPWLGVGMWQ
FT	(in isoform 4).
FT	/FtId-VSP_004557.
FT	MEPTVPSERSLSLSLPFGREGATLKPPQHLWRQPRTPI
FT	RIOQRGYSDSAERAERQPHRIERADAMDTSDRPLGRIT
FT	RMWPSPFHGTGTGGAGGSSRRFEANGPTTSPGRSPL
FT	DSQAQGLVLHAGAATSORRESFLYSDSDYDMSPKTMSRN
FT	SVVTSABAHDLIVTPFAQVLASLRSVRNSFSLLTNVVPVS
FT	NKESPLGGPVPCKATLSEETCOQLARETELELDWCLEOLE
FT	TMTYISVSEMASHK -> MPLVDFFCETCSKPWLGVGMWQ
FT	(in isoform 4).
FT	/FtId-VSP_004558.
FT	MEPTVPSERSLSLSLPFGREGATLKPPQHLWRQPRTPI
FT	RIOQRGYSDSAERAERQPHRIERADAMDTSDRPLGRIT
FT	RMWPSPFHGTGTGGAGGSSRRFEANGPTTSPGRSPL
FT	DSQAQGLVLHAGAATSORRESFLYSDSDYDMSPKTMSRN
FT	SVVTSABAHDLIVTPFAQVLASLRSVRNSFSLLTNVVPVS
FT	NKESPLGGPVPCKATLSEETCOQLARETELELDWCLEOLE
FT	TMTYISVSEMASHKFRMLNRLTHLSEMSRSGNQVSEYI
FT	STTFLLDKQNEVEIPSPTMKEREQQAAPRPSPPPPVPFH
FT	LQPMQTITGLIKMLHSNLNSNIIPRFVGKTDOELLAQ
FT	-> MVLPSDDGXKLGNLVLCQPPRYRLTLTSGLRHLQ (in
FT	isoform 5).
FT	/FtId-VSP_004559.
FT	GFDIYLHPULWETM -> QARGIDGRAQQGFY (in
FT	isoform 5).
FT	/FtId-VSP_004560.
FT	Missing (in isoform 5).
FT	/FtId-VSP_004561.
FT	E -> A (IN REF. 1, 2, 6; AAB33798 AND 7).
FT	886 AA; 98201 MW; 483EDF9BA9756CA CRC64;
SQ	SEQUENCE
Query Match	24.1%; Score 541; DB 1; Length 886;
Best Local Similarity	32.3%; Pred. No. 1.6e-36;
Matches 124; Conservative	69; Mismatches 159; Indels 32; Gaps 6;
QY	22 ESRERGSH-PYIDFRIFHSQSIEVSVSNRNTIRLLSFOR-----YLRSSRF 67
DB	275 EMRSRGNGVSEYSTTTFLDKQNEVEIPSPTMKEREQQAAPRPSPPPPVPFHLPQMSQ 334
QY	68 FRGTAV---SNSINI-----LDDDYNGOAKCMLEKVGNWNPNDFLFDRLTNGNSLVSL 117
Db	335 ITGIKKIMHSNINSNNIPREGVKTKTOEFLLAOFENIKWKGINICVSDYAGGSPTCTI 394


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FT VARSPLIC 1 167 Missing (in isoform 3).
FT CONFLICT 95 95 /FTIC-VSP_004582.
FT CONFLICT 349 355 MISSING (IN REF. 3).
FT CONFLICT 510 510 G -> E (IN REF. 3).
FT CONFLICT 626 626 C -> Y (IN REF. 3).
SQ SEQUENCE 672 AA; 76263 MW; 63CE38FA654A0BDD CRC64;

Query Match 24.0%; Score 539; DB 1; Length 672;
Best Local Similarity 31.6%; Pred. No. 1.6e-36;
Matches 122; Conservative 81; Mismatches 151; Indels 32; Gaps 7;

QY 8 RMLGDRVRSRAGFESRERGHYPIDFRIFHSQSELEV-----SVSARNIRLLSPQ 59
DB 178 RELTHLSEMSRSGNQVSEIYSITFLD-----KQHEVEIESPQKEKKRPMQISGVK 232
QY 60 RYLRSRFRPGTAVNS-----NLMLDDDDYQAKCMLEKVGNNWDFIFLFLDTNGNSLV 115
DB 233 KLHSS-----SLTNSCIPRGVKTQEDVLAK-ELEDVNWGLHVFRIAEISGNRPLT 285
QY 116 SUTFLHSLHGLIEVHLMKRLRLVMIQDYSQNPYHNAHADVTQAMHCYLKEP 175
DB 286 VIMHTIFQERDLKTPKIPVDITLITMTLEHDYHADVAHHNIHAADVQSTHLLSTP 345
QY 176 KLANSTPMDIILLSLAAATHLDHPGVNQPFLLKTNHYLATLYKNTSVLENHHRSAVG 235
DB 346 ALEAVFTDLEILAAIPASAIHVDHVEGVNQFLINTNSALMYNDSSVLENHHLAVGFK 405
QY 236 LLRESG--LFSHLPLESROQMETQIGALILATDISRQNEYLSLFRSHLD-----RGDLIC 287
DB 406 LLQEENCDFIQLTKQORSLRQWADIVLATDMSKHMNLADLTKMTVETKKTSSGVLL 465
QY 288 LEDTRHRLHVLQALCAIDICNPTWELSKQSEKVTPEFFHOGDIEKKYHLGVSPICD 347
DB 466 LONYSRIQVLQNVHCAIDNSNPTKPLQYRQWTDRIEMEFPFQGRERERGMETSPMCD 525
QY 348 RUTESANTIQIGMTYVEPLFTWA 373
DB 526 KHNASVEKSGVGFIDIVHPLWETWA 551

RESULT 14
CN4C_RAT STANDARD; PRT; 536 AA.
AC P14644;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CAMP-specific 3',5'-cyclic phosphodiesterase 4C (EC 3.1.4.17)
DE (DPDE1) (Fragment).
GN PDE4C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95047482; PubMed=7958996;
RA Bolger G.B., Rodgers L., Riggs M.;
RT "Differential CNS expression of alternative mRNA isoforms of the
RL mammalian genes encoding cAMP-specific phosphodiesterases.";
RL Gene 149:237-244 (1994).
RN [2]
RP SEQUENCE OF 153-511 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=89315790; PubMed=2546153;
RA Swinnen J.V., Joseph D.R., Conti M.;
RT "Molecular cloning of rat homologues of the Drosophila melanogaster
RL duncce cAMP phosphodiesterase: evidence for a family of genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329 (1989).
CC CC -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC adenosine 5'-phosphate.
CC -!- ENZYME REGULATION: Inhibited by rolipram.

```

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CC CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC family.
CC
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CC
CC -----
CC EMBL; L27061; AAA56858.1; -.
CC EMBL; M25347; AAA41847.1; -.
CC PIR; I67945; I67945.
CC InterPro; IPR003607; Met_phosphohydro.
CC InterPro; IPR002073; PDEase.
CC Pfam; PF00233; PDEase; 1.
CC PRINTS; PR00387; PDIESTERASE1.
CC SMART; SM00471; Hdc; 1.
CC PROSITE; PS00126; PDEASE_1; 1.
KW Hydrolase; CAMP; Multigene family.
FT NON TER 1 1
FT DOMAIN 524 534 POLY-GLU.
FT CONFLICT 218 218 R -> S (IN REF. 2).
FT CONFLICT 507 507 S -> N (IN REF. 2).
FT CONFLICT 536 AA; 60063 MW; 87D12BE2C46642F3 CRC64;
SQ SEQUENCE 536 AA; 60063 MW; 87D12BE2C46642F3 CRC64;

Query Match 23.8%; Score 534.5; DB 1; Length 536;
Best Local Similarity 32.2%; Pred. No. 2.8e-36;
Matches 118; Conservative 71; Mismatches 159; Indels 19; Gaps 6;

QY 22 ESRGSH--PYDFRIFHSQSEIEVSVSARN-----IRRLSFKYLRSSFRFGTAVS 74
DB 117 ETSRSGNVSEVISOTFLDQQAQAEVLPAPPTEDHPWPAQITGLKRSCHTS---LPTAAI 173
QY 75 NSLNLDDDDYQAKCMLEKVGNNWDFIFLFLDTNGNSLVSLTFLHSLHGLIEVFFHLD 134
DB 174 PRFGVTDQEEQLAK-ELEDTKWGLDVPKVAELSGNRPLTAVIFVLQERDLTKTQIP 232
QY 135 MKLRLRFLVMIQEDYHSQNPYHNAHADVTQAMHCYLKEPKLANSVTPDILLSLIAAA 194
DB 233 ADTLRYLLTLEGHVSNVAYHNSIHAADVQSAHVLLGTLPALAEVFTDLEVLALFACA 292
QY 195 THDLDPGVNQPFLLKTNHYLATLYKNTSVLENHHRSAVGLIR--ESGLFSLPLESKQ 252
DB 293 IHDVDPGVNQFLINTNSALMYNDSSVLENHHLAVGFKLLQGENCDFQNLSTKQKL 352
QY 253 QMETQIGALILATDISRQNEYLSPFRSHLD-----GDLCIEDTRHRLHVLQALKCAD 306
DB 353 SLRRWVIDMVLATDMSKMSLLADLTKMTVETKVTSLGLVLLDNDYSDRIQVLSLVHCD 412
QY 307 ICNPCRTWELSKQSEKVTPEFFHOGDIEKKYHLGVSPICDRHTESIAMIQIGMTYVE 366
DB 413 LSNPAKPLFYRQWTERIMAEFFQGRERESGLDISPMCDKHTASVEKSGVGFIDYIAH 472
QY 367 PLFTWA 373
DB 473 PLWETWA 479

RESULT 15
CN8A_HUMAN STANDARD; PRT; 829 AA.
ID CN8A_HUMAN Q96911; Q96PD0; Q96PD1; Q9UMB7;
AC Q96911; Q96911; Q96911; Q96911; Q96911; Q96911; Q96911; Q96911;
DT 18-JUL-1999 (Rel. 38, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE High-affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic
DE phosphodiesterase 8A (EC 3.1.4.17).
GN PDE8A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4-5).
 RC TISSUE=Testis;
 RX MEDLINE=21601118; PubMed=11738832;
 RA Wang P., Wu P., Egan R.W., Billah M.M.;
 RT "Human phosphodiesterase 8A splice variants: cloning, gene
 RT organization, and tissue distribution.";
 RL Gene 280:183-194(2001).
 RN [2]
 RN SEQUENCE OF 117-929 FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=98289571; PubMed=9618252;
 RA Fisher D.A., Smith J.F., Pillar J.S., St Denis S.H., Cheng J.B.;
 RT "Isolation and characterization of PDE8A, a novel human cAMP-specific
 RT phosphodiesterase.";
 RL Biochem. Biophys. Res. Commun. 246:570-577(1998).
 RN [3]
 RN SEQUENCE OF 670-929 FROM N.A.
 RA Carim L., Estivill X., Sumoy L., Escarceller M.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Plays a role in signal transduction by regulating the
 CC intracellular concentration of cyclic nucleotides. This
 CC phosphodiesterase, which has a high affinity for cAMP, may be
 CC involved in maintaining basal levels of the cyclic nucleotide
 CC and/or in the cAMP regulation of germ cell development.
 CC -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
 CC adenosine 5'-phosphate.
 CC -!- COFACTOR: Requires divalent cations. Magnesium or manganese are
 CC required for maximum activity, in vitro.
 CC -!- ENZYME REGULATION: Inhibited by dipyrdimole. Insensitive to
 CC selective PDE inhibitors including rolipram and zaprinast as well
 CC as to the non-selective inhibitor, IBMX. Unaffected by cGMP.
 CC -!- PATHWAY: Cyclic nucleotide metabolism.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=PDE8A1;
 CC IsoId=O60658-1; Sequence=Displayed;
 CC Name=2; Synonyms=PDE8A2;
 CC IsoId=O60658-2; Sequence=VSP_004597;
 CC Name=3; Synonyms=PDE8A3;
 CC IsoId=O60658-3; Sequence=VSP_004596;
 CC Name=4-5; Synonyms=PDE8A4, PDE8A5;
 CC IsoId=O60658-4; Sequence=VSP_004595;
 CC -!- TISSUE SPECIFICITY: Expressed in most tissues except thymus and
 CC peripheral blood leukocytes. Highest levels in testis, ovary,
 CC small intestine and colon.
 CC -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
 CC putative divalent metal sites and an N-terminal regulatory domain.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
 CC family.
 CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
 CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
 CC -----
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 CC -----
 CC EMBL; AF388183; AAL18610.1; -
 CC EMBL; AF388184; AAL18611.1; -
 CC EMBL; AF388185; AAL18612.1; -
 CC EMBL; AF388186; AAL18613.1; -
 CC EMBL; AF388187; AAL18614.1; -
 CC EMBL; AF056490; AAC39763.1; -
 CC EMBL; AAL109687; CAB52020.1; -
 CC FIR; JWC088; JWC0088.
 CC Genew; HGNC:8793; PDE8A.
 CC MIM; 602972; -
 CC GO; GO:0004114; F:3; 5'-cyclic-nucleotide phosphodiesterase a. . .; NAS.

DR GO:0009187; P:cyclic nucleotide metabolism; NAS.
 DR InterPro; IPR003607; Met_phosphohydro.
 DR InterPro; IPR000014; PAS_domain.
 DR InterPro; IPR002073; PDEase.
 DR Pfam; PF00989; PAS; 1.
 DR Pfam; PF00233; PDEase; 1.
 DR PRINTS; PR00387; PDIESTERASE1.
 DR SMART; SM00471; HDG; 1.
 DR SMART; SM00091; PAS; 1.
 DR TIGRFAMs; TIGR00229; sensory_box; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 DR PROSITE; PS01112; PAS; 1.
 KW Hydrolase; cAMP; Alternative splicing; Manganese; Magnesium;
 KW Multigene family.
 FT DOMAIN 213 283 PAS.
 FT DOMAIN 287 329 PAC.
 FT METAL 531 556 MAGNESIUM OR MANGANESE 1 (POTENTIAL).
 FT METAL 560 560 MAGNESIUM OR MANGANESE 1 (POTENTIAL).
 FT METAL 585 585 MAGNESIUM OR MANGANESE 1 (POTENTIAL).
 FT METAL 596 596 MAGNESIUM OR MANGANESE 2 (POTENTIAL).
 FT METAL 600 600 MAGNESIUM OR MANGANESE 2 (POTENTIAL).
 FT METAL 626 626 MAGNESIUM OR MANGANESE 2 (POTENTIAL).
 FT VARSPLIC 1 247 Missing (in isoform 4-5).
 FT VARSPLIC 1 380 Missing (in isoform 3).
 FT VARSPLIC 239 284 Missing (in isoform 2).
 FT CONFLICT 344 344 H -> R (IN REF. 2).
 FT CONFLICT 399 399 I -> V (IN REF. 2).
 SQ SEQUENCE 829 AA; 93303 MW; 99BD05EA185A42CD CRC64;
 Query Match 22.4%; Score 503; DB 1; Length 829;
 Best Local Similarity 31.6%; Pred. No. 1.9e-33;
 Matches 117; Conservative 76; Mismatches 145; Indels 32; Gaps 7;
 QY 54 RLSPQYLRSSRRFRGTAVNSLMLD---DYNGQAKCMLEKVGNNWDFILFDRLT 109
 DB 454 RRLSGNEVLSI---KNTQMVS---NIITPISLDDVFPRIARAMEEYWDFFILEEAT 509
 QY 110 NGNSIVSLTFHLSHLGLIEYFHLDMKRLRFLVMIQEDYHSQNPYHNAHVADVTQAMH 169
 DB 510 HNRPLIYLGLKMFARFGICEFLRCSESTLRSMLQIIEANYHSSNPYHNSHDSADVLHATA 569
 QY 170 CYLKEPKLANSVTPWDILLSLIAAATHDLDPGVNQPELIKTNHYLATYKNTSVLENHH 229
 DB 570 YFLSKERIKETIDPDIDEVAALIAATHDVPGRNTSNFLCNAGSELAIYNDTAVLESHH 629
 QY 230 WRSVAVGLLR---ESGLFSLPLESRQOMETQCALILATDISRQNEYLSLFRSHLDGRDL 286
 DB 630 AALAQLTITGDDKCNIFKNMERNDYRTLQGIIDVLTATEMTKFEHVKNFVNSINKPLA 689
 QY 287 CLEDT-----RHHLVLQALKACIDICNPORTELWELSKQSEKVTHERFF 329
 DB 690 TLENGETDKNQEVINTMLRTPENRTLIKRMLIKADVSNPCRPLOQYCIENWARISEYF 749
 QY 330 HQGDIEKKYHLG-VSPLCDRHTEIANIQIGPWYLVLEPLFTEWAFRSNLTSLQTMGLHV 388
 DB 750 SQTDEKQOGLPVMFVDFRNTCSIPKSQLSFIDYFITDMFADAFVDL---PDLNQHL 806
 QY 389 GLNKASWKL 398
 DB 807 DNNFYWKGL 816
 Search completed: May 26, 2004, 09:25:02
 Job time : 19 secs

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OM protein - protein search, using sw model

Run on: May 26, 2004, 09:26:43 ; Search time 577 Seconds
(without alignments)
205.928 Million cell updates/sec

Title: US-09-966-781A-1
Perfect score: 2243
Sequence: 1 DOTALYRMLGDVVRSGAG.....DTDAFAELNSQLPQENRLS 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1149313 seqs, 278921704 residues

Total number of hits satisfying chosen parameters: 1149313

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/BCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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- 6: /cgn2_6/ptodata/1/pubpaa/PTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2243	100.0	426	10	US-09-966-781A-1
2	2116	94.3	426	10	US-09-966-781A-3
3	2105	93.8	426	10	US-09-966-781A-2
4	1903	84.8	432	9	US-09-764-898-208
5	1787	79.7	336	14	US-10-258-746-2
6	1383.5	61.7	502	12	US-10-311-104-1
7	1383.5	61.7	502	14	US-10-273-517-1
8	1383.5	61.7	502	15	US-10-386-414-4
9	1079	48.1	211	9	US-09-764-898-280
10	1079	48.1	211	10	US-09-989-442-120
11	871	38.8	320	15	US-10-386-414-6
12	555	24.7	610	14	US-10-627-970-17
13	555	24.7	610	15	US-10-627-929-9
14	551	24.6	721	12	US-09-983-754-2
15	550	24.5	517	16	US-10-442-675-2

16	550	24.5	564	9	US-09-947-305-2	Sequence 2, Appli
17	550	24.5	564	12	US-09-983-754-4	Sequence 4, Appli
18	550	24.5	564	14	US-10-076-597-48	Sequence 48, Appl
19	550	24.5	564	14	US-10-205-219-19	Sequence 19, Appl
20	550	24.5	564	15	US-10-149-536-8	Sequence 8, Appli
21	550	24.5	657	12	US-10-087-192-1629	Sequence 1629, Ap
22	550	24.5	659	15	US-10-149-536-2	Sequence 2, Appli
23	550	24.5	721	12	US-10-087-192-1632	Sequence 1632, Ap
24	550	24.5	721	15	US-10-149-536-9	Sequence 9, Appli
25	550	24.5	736	15	US-10-149-536-6	Sequence 6, Appli
26	550	24.5	736	15	US-10-149-536-7	Sequence 7, Appli
27	544	24.3	1124	14	US-10-257-909A-6	Sequence 6, Appli
28	542	24.2	507	14	US-10-076-597-49	Sequence 49, Appl
29	542	24.2	507	14	US-10-067-514-10	Sequence 10, Appl
30	542	24.2	507	15	US-10-419-723-10	Sequence 10, Appl
31	542	24.2	517	12	US-10-165-135-6	Sequence 6, Appli
32	542	24.2	517	12	US-10-703-939-6	Sequence 6, Appli
33	542	24.2	517	12	US-10-704-447-6	Sequence 6, Appli
34	542	24.2	564	12	US-10-165-135-5	Sequence 5, Appli
35	542	24.2	564	12	US-10-703-939-5	Sequence 5, Appli
36	542	24.2	564	12	US-10-704-447-5	Sequence 5, Appli
37	542	24.2	585	14	US-10-067-514-9	Sequence 9, Appli
38	542	24.2	585	15	US-10-419-723-9	Sequence 9, Appli
39	542	24.2	673	14	US-10-076-597-51	Sequence 51, Appl
40	542	24.2	673	14	US-10-067-514-6	Sequence 6, Appli
41	542	24.2	673	15	US-10-419-723-6	Sequence 6, Appli
42	542	24.2	687	14	US-10-239-439-4	Sequence 4, Appli
43	542	24.2	687	14	US-10-067-514-8	Sequence 8, Appli
44	542	24.2	687	15	US-10-419-723-8	Sequence 8, Appli
45	542	24.2	721	12	US-10-165-135-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-966-781A-1
; Sequence 1, Application US/099666781A
; Publication No. US20030036184A1
; GENERAL INFORMATION: PATRICIA
; APPLICANT: SOULARD, PATRICIA
; TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR
; TITLE OF INVENTION: SELECTING COMPOUNDS WHICH INHIBIT PDE7 ENZYME ACTIVITY
; FILE REFERENCE: A0000281US
; CURRENT APPLICATION NUMBER: US/09/966,781A
; PRIOR FILING DATE: 2004-09-28
; PRIOR APPLICATION NUMBER: EP004026837
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 1
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-781A-1

Query Match	100.0%;	Score 2243;	DB 10;	Length 426;
Best Local Similarity	100.0%;	Pred. No. 3.1e-225;		
Matches 426;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	DOTALYRMLGDVVRSGAGFESRRGSHPYIDFRIFHSSQSETEVSVSARNIRLLS	FOR 60	
Db	1	DOTALYRMLGDVVRSGAGFESRRGSHPYIDFRIFHSSQSETEVSVSARNIRLLS	FOR 60	
Qy	61	YLSSFFFRGTAVSNSINILDDYNGQAKCMLEKGVNWNFDIFLFRLTNGNSIVSLTFH	120	
Db	61	YLSSFFFRGTAVSNSINILDDYNGQAKCMLEKGVNWNFDIFLFRLTNGNSIVSLTFH	120	
Qy	121	LFSLHGLIEYFHLDMKKRLFLVMIQEDYHSQNPYHNAHAADVTQAMHCYLPKPKLANS	180	
Db	121	LFSLHGLIEYFHLDMKKRLFLVMIQEDYHSQNPYHNAHAADVTQAMHCYLPKPKLANS	180	
Qy	181	VTPWDILLSIAAATHDLDHPGVNQPLIKTNHYLTLYKNTSVLENHWRSAVGLLR	240	

Db 181 VTPWDILLSIAAAATDLDHPGVNPFLLIKTNHYLATYKNTSVLENHHRSAVGLLRES 240
 QY 241 GLFSLPLESRQOMETOIGALILATDISRQNEVLSLFRSHLDGRDCLDTRHRLVLM 300
 Db 241 GLFSLPLESRQOMETOIGALILATDISRQNEVLSLFRSHLDGRDCLDTRHRLVLM 300
 QY 301 ALKCADICNPCTWELSKQWSEKVTTEFFHQGDIEKKYHLGVSPICDRHTESIANIQIGF 360
 Db 301 ALKCADICNPCTWELSKQWSEKVTTEFFHQGDIEKKYHLGVSPICDRHTESIANIQIGF 360
 QY 361 MTYLVEPLFTWARFNSNTRLSQTMGLGVGNKASWKGLOREOSSDITDAAAFELNSQLLP 420
 Db 361 MTYLVEPLFTWARFNSNTRLSQTMGLGVGNKASWKGLOREOSSDITDAAAFELNSQLLP 420
 QY 421 QENRLS 426
 Db 421 QENRLS 426
 RESULT 2
 US-09-966-781A-3
 ; Sequence 3, Application US/09966781A
 ; Publication No. US20030036184A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SOULARD, PATRICIA
 ; TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR
 ; FILE REFERENCE: A0000281US
 ; CURRENT APPLICATION NUMBER: US/09/966,781A
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: EP004026837
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 426
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 US-09-966-781A-3
 Query Match 94.3%; Score 2116; DB 10; Length 426;
 Best Local Similarity 94.1%; Pred. No. 5.8e-212;
 Matches 401; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
 QY 1 DOTALYIRMLGDVVRVRAGFESERRGSHPIYDFRIFHSQSEIEVSASRNIRLLSFQR 60
 Db 1 DOTALYIRMLGDVVRVRAGFESERRGSHPIYDFRIFHSQSEIEVSASRNIRLLSFQR 60
 QY 61 YLRSSRFRGTAVSNSNILLDDYNGQAKCMLEKVGNNWFDFLFDRLTNGNSLVSLTFH 120
 Db 61 YLRSSRFRGTAVSNSNILLDDYNGQAKCMLEKVGNNWFDFLFDRLTNGNSLVSLTFH 120
 QY 121 LFSHLGLIEYFHLDMVKLRFLVMIOEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
 Db 121 LFSHLGLIEYFHLDMVKLRFLVMIOEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
 QY 181 VTPWDILLSIAAAATDLDHPGVNPFLLIKTNHYLATYKNTSVLENHHRSAVGLLRES 240
 Db 181 VTPWDILLSIAAAATDLDHPGVNPFLLIKTNHYLATYKNTSVLENHHRSAVGLLRES 240
 QY 241 GLFSLPLESRQOMETOIGALILATDISRQNEVLSLFRSHLDGRDCLDTRHRLVLM 300
 Db 241 GLFSLPLESRQOMETOIGALILATDISRQNEVLSLFRSHLDGRDCLDTRHRLVLM 300
 QY 301 ALKCADICNPCTWELSKQWSEKVTTEFFHQGDIEKKYHLGVSPICDRHTESIANIQIGF 360
 Db 301 ALKCADICNPCTWELSKQWSEKVTTEFFHQGDIEKKYHLGVSPICDRHTESIANIQIGF 360
 QY 361 MTYLVEPLFTWARFNSNTRLSQTMGLGVGNKASWKGLOREOSSDITDAAAFELNSQLLP 420
 Db 361 MTYLVEPLFTWARFNSNTRLSQTMGLGVGNKASWKGLOREOSSDITDAAAFELNSQLLP 420

QY 421 QENRLS 426
 Db 421 QENRLS 426
 RESULT 3
 US-09-966-781A-2
 ; Sequence 2, Application US/09966781A
 ; Publication No. US20030036184A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SOULARD, PATRICIA
 ; TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR
 ; FILE REFERENCE: A0000281US
 ; CURRENT APPLICATION NUMBER: US/09/966,781A
 ; CURRENT FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: EP004026837
 ; PRIOR FILING DATE: 2000-09-28
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 426
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-09-966-781A-2
 Query Match 93.8%; Score 2105; DB 10; Length 426;
 Best Local Similarity 93.7%; Pred. No. 8.2e-211;
 Matches 399; Conservative 13; Mismatches 14; Indels 0; Gaps 0;
 QY 1 DOTALYIRMLGDVVRVRAGFESERRGSHPIYDFRIFHSQSEIEVSASRNIRLLSFQR 60
 Db 1 DOTALYIRMLGDVVRVRAGFESERRGSHPIYDFRIFHSQSEIEVSASRNIRLLSFQR 60
 QY 61 YLRSSRFRGTAVSNSNILLDDYNGQAKCMLEKVGNNWFDFLFDRLTNGNSLVSLTFH 120
 Db 61 YLRSSRFRGTAVSNSNILLDDYNGQAKCMLEKVGNNWFDFLFDRLTNGNSLVSLTFH 120
 QY 121 LFSHLGLIEYFHLDMVKLRFLVMIOEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
 Db 121 LFSHLGLIEYFHLDMVKLRFLVMIOEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
 QY 181 VTPWDILLSIAAAATDLDHPGVNPFLLIKTNHYLATYKNTSVLENHHRSAVGLLRES 240
 Db 181 VTPWDILLSIAAAATDLDHPGVNPFLLIKTNHYLATYKNTSVLENHHRSAVGLLRES 240
 QY 241 GLFSLPLESRQOMETOIGALILATDISRQNEVLSLFRSHLDGRDCLDTRHRLVLM 300
 Db 241 GLFSLPLESRQOMETOIGALILATDISRQNEVLSLFRSHLDGRDCLDTRHRLVLM 300
 QY 301 ALKCADICNPCTWELSKQWSEKVTTEFFHQGDIEKKYHLGVSPICDRHTESIANIQIGF 360
 Db 301 ALKCADICNPCTWELSKQWSEKVTTEFFHQGDIEKKYHLGVSPICDRHTESIANIQIGF 360
 QY 361 MTYLVEPLFTWARFNSNTRLSQTMGLGVGNKASWKGLOREOSSDITDAAAFELNSQLLP 420
 Db 361 MTYLVEPLFTWARFNSNTRLSQTMGLGVGNKASWKGLOREOSSDITDAAAFELNSQLLP 420
 QY 421 QENRLS 426
 Db 421 QENRLS 426
 RESULT 4
 US-09-966-898-208
 ; Sequence 208, Application US/09764898
 ; Patent No. US20020090673A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSEN ET AL.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: R201
 ; CURRENT APPLICATION NUMBER: US/09/764,898
 ; CURRENT FILING DATE: 2001-01-17

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; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 208
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (419)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-208

Query Match      84.8%; Score 1903; DB 9; Length 432;
Best Local Similarity 99.2%; Pred. No. 1.1e-189;
Matches 361; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DOTATYIRMLGADVVRGRAGFESERRGSHPIYDFRIFHSQSEIEVSVSARNIRLLSFQR 60
DB 65 DOTATYIRMLGADVVRGRAGFESERRGSHPIYDFRIFHSQSEIEVSVSARNIRLLSFQR 124
QY 61 YLRSSRRFRGTAVERNLSNMLDDYNGQAKCMLEKVGNNWFDIFLDRITNGNSLVSTFFH 120
DB 125 YLRSSRRFRGTAVERNLSNMLDDYNGQAKCMLEKVGNNWFDIFLDRITNGNSLVSTFFH 184
QY 121 LFSHLGLIEYFHLDMKLRRLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
DB 185 LFSHLGLIEYFHLDMKLRRLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 244
QY 181 VTPDWILLSLIAAATHDHPGVNQPFLLIKTNHYLATLYKNTSVLENHHRWSAVGLLRES 240
DB 245 VTPDWILLSLIAAATHDHPGVNQPFLLIKTNHYLATLYKNTSVLENHHRWSAVGLLRES 304
QY 241 GLFSLPLSRQOMETQIGALILATDISRQNEYLSLFRSHLDGRGDLCELTDRHRHLVLM 300
DB 305 GLFSLPLSRQOMETQIGALILATDISRQNEYLSLFRSHLDGRGDLCELTDRHRHLVLM 364
QY 301 ALKCADICNPCTWELSKQSEKVTPEEPHQDIEKKYHLGVSPICDRHTESIANGIQIF 360
DB 365 ALKCADICNPCTWELSKQSEKVTPEEPHQDIEKKYHLGVSPICDRHTESIANGIQION 424
QY 361 MYTL 364
DB 425 YTYL 428

RESULT 5
US-10-258-746-2
; Sequence 2, Application US/10258746
; Publication No. US20030138815A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: New Phosphodiesterase type 7
; FILE REFERENCE: PDE7spliceFWKS
; CURRENT APPLICATION NUMBER: US/10/258,746
; CURRENT FILING DATE: 2002-10-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-746-2

Query Match      79.7%; Score 1787; DB 14; Length 336;
Best Local Similarity 100.0%; Pred. No. 9.7e-178;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 MLEKVGNNWFDIFLDRITNGNSLVSTFHLFSLHGLIEYFHLDMKLRRLVMIQEDYH 150
DB 1 MLEKVGNNWFDIFLDRITNGNSLVSTFHLFSLHGLIEYFHLDMKLRRLVMIQEDYH 60
QY 151 SQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSIAAATHDHPGVNQPFLLIK 210

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DB 61 SQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSIAAATHDHPGVNQPFLLIK 120
QY 211 TNYHLATLYKNTSVLENHHRWSAVGLLRESGLFSLHPLSRQOMETQIGALILATDISRQ 270
DB 121 TNYHLATLYKNTSVLENHHRWSAVGLLRESGLFSLHPLSRQOMETQIGALILATDISRQ 180
QY 271 NEYLSLFRSHLDGRGDLCELTDRHRHLVLMALKCADICNPCTWELSKQSEKVTPEFFH 330
DB 181 NEYLSLFRSHLDGRGDLCELTDRHRHLVLMALKCADICNPCTWELSKQSEKVTPEFFH 240
QY 331 QGDIKKYHLGVSPICDRHTESIANGIQIFGNTYLVLEPLFTFEWARFNSNTRLSQTMGLHVL 390
DB 241 QGDIKKYHLGVSPICDRHTESIANGIQIFGNTYLVLEPLFTFEWARFNSNTRLSQTMGLHVL 300
QY 391 NKASWKGLOREQSSSEDTDAAFELNSQLLPQENRLS 426
DB 301 NKASWKGLOREQSSSEDTDAAFELNSQLLPQENRLS 336

RESULT 6
US-10-311-104-1
; Sequence 1, Application US/10311104
; Publication No. US20040054138A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: THORNTON, Michael
; APPLICANT: DING, Li
; APPLICANT: ARIZU Chandra S.
; APPLICANT: YAO, Monique G.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: LAL, Preeti G.
; APPLICANT: HAFALIA, April J. A.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: LU, Yan
; APPLICANT: Chawla, Narinder K.
; TITLE OF INVENTION: PHOSPHODIESTERASES
; FILE REFERENCE: PI-0136 PCT
; CURRENT APPLICATION NUMBER: US/10/311,104
; CURRENT FILING DATE: 2002-12-12
; PRIOR APPLICATION NUMBER: PCT/US01/20140
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/213,741
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/218,234
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/241,100
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040054138A1 7476201CD1
US-10-311-104-1

Query Match      61.7%; Score 1383.5; DB 12; Length 502;
Best Local Similarity 62.9%; Pred. No. 2.6e-135;
Matches 253; Conservative 65; Mismatches 83; Indels 1; Gaps 1;

QY 11 GDRVRSRAGFESERRGSHPIYDFRIFHSQSEIEVSVSARNIRLLSFQRYSRRFFRG 70
DB 80 GDIRLFGQGVRAERRGSYPFDIFRLNLTSTTSGEIGTKKKVKRLLSFQRYPHASLLRG 139
QY 71 TAVSNSINTLDDYNGQAKCMLEKVGNNWFDIFLDRITNGNSLVSTFHLFSLHGLIEY 130
DB 140 IIPQAPHLHLLDEYLGQARHMLSKVGWDFDIFLDRITNGNSLVSTFHLFSLHGLIEY 199
QY 131 FHLDMKLRRLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLS 190

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Db 200 FKLDVTLHRFLVMQEDYHSQPNYHNAVHAADVTQAMHCYLUKEXPLAFLPLDMLGL 259
QY 191 IAAATHDLDHPGVNQDFLLKTNHYLATYKNTSVLENHWRSAVGLLRSGFLSHLPLES 250
Db 260 LAAAHADVHPGVNQDFLLKTNHHLANLYQNMVLENHWRSTIGMLRESRLLAHLPKEM 319
QY 251 RQOMETQICALLIATDISRQNEYLSFRSHLDRGDLCLEDTTHRHVLVQALKACADICNP 310
Db 320 TDIEQOGLSLLIATDINRQNEFLTRKKAHLNKKLRLEDAQDRHFMQLQALKACADICNP 379
QY 311 CRTWELSKQSEKVTFFHOGDIEKKYHGVSPICDRHTESIANIQTIGFMTYLVPELFT 370
Db 380 CRWELSKQSEKVTFFHOGDIEKKYHGVSPICDRHTESIANIQTIGFMTYLVPELFT 439
QY 371 EWARFS-NTRLSTQMLGHVGLNKASKWGLQREQSSSEDTDA 411
Db 440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSGSGS 481

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RESULT 7

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US-10-273-517-1
; Sequence 1, Application US/10273517
; Publication No. US20030143588A1
; GENERAL INFORMATION:
; APPLICANT: THORNTON, Michael B.; DING, Li
; APPLICANT: ARVIZU, Chandra S.; YAO, Monique G.
; APPLICANT: TRIBOULEY, Catherine M.; LAL, Preeti G.
; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.
; APPLICANT: RAMKUMAR, Javalaxmi; LU, Yan
; APPLICANT: CHAWLA, Nariender K.
; TITLE OF INVENTION: PHOSPHODIESTERASES
; FILE REFERENCE: PI-0136 USA
; CURRENT APPLICATION NUMBER: US/10/273,517
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 60/241,100
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/218,234
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US01/20140
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/213,741
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030143588A1 7476201CD1
US-10-273-517-1

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Query Match 61.7%; Score 1383.5; DB 14; Length 502;
Best Local Similarity 62.9%; Pred. No. 2.6e-135;
Matches 253; Conservative 65; Mismatches 83; Indels 1; Gaps 1;

QY 11 GGVVRASRAGFESRRGSHPYIDFRIFHSQSEIEVSVSARNIRLLSFQRYLRSSFFRG 70
Db 80 GDRLRGQTVRAERGRSYPFIDFRLNLTYSYGEIGTKKKVKRLLSFQRYFHASRLRG 139
QY 71 TAVSNSINLDDYNGQAKMELKGVGNWFDIFDLRLTNGSLVSLTFLHSLGLIEY 130
Db 140 IIPQAPLHLDDEYLGQARHMLSKVGMWDFIDFLDLRLTNGSLVSLTFLHSLGLIEY 199
QY 131 FHLDMKRLRFLVMIQDYHSQPNYHNAVHAADVTQAMHCYLUKEXPLAFLPLDMLGL 190
Db 200 FKLDVTLHRFLVMQEDYHSQPNYHNAVHAADVTQAMHCYLUKEXPLAFLPLDMLGL 259
QY 191 IAAATHDLDHPGVNQDFLLKTNHYLATYKNTSVLENHWRSAVGLLRSGFLSHLPLES 250
Db 260 LAAAHADVHPGVNQDFLLKTNHHLANLYQNMVLENHWRSTIGMLRESRLLAHLPKEM 319

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QY 251 RQOMETQICALLIATDISRQNEYLSFRSHLDRGDLCLEDTTHRHVLVQALKACADICNP 310
Db 320 TDIEQOGLSLLIATDINRQNEFLTRKKAHLNKKLRLEDAQDRHFMQLQALKACADICNP 379
QY 311 CRTWELSKQSEKVTFFHOGDIEKKYHGVSPICDRHTESIANIQTIGFMTYLVPELFT 370
Db 380 CRWELSKQSEKVTFFHOGDIEKKYHGVSPICDRHTESIANIQTIGFMTYLVPELFT 439
QY 371 EWARFS-NTRLSTQMLGHVGLNKASKWGLQREQSSSEDTDA 411
Db 440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSGSGS 481

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RESULT 8

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US-10-386-414-4
; Sequence 4, Application US/10386414
; Publication No. US20040006016A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
; FILE REFERENCE: ME103-0210NMIM
; CURRENT APPLICATION NUMBER: US/10/386,414
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/833,082
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-386-414-4

```

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Query Match 61.7%; Score 1383.5; DB 15; Length 502;
Best Local Similarity 62.9%; Pred. No. 2.6e-135;
Matches 253; Conservative 65; Mismatches 83; Indels 1; Gaps 1;

QY 11 GGVVRASRAGFESRRGSHPYIDFRIFHSQSEIEVSVSARNIRLLSFQRYLRSSFFRG 70
Db 80 GDRLRGQTVRAERGRSYPFIDFRLNLTYSYGEIGTKKKVKRLLSFQRYFHASRLRG 139
QY 71 TAVSNSINLDDYNGQAKMELKGVGNWFDIFDLRLTNGSLVSLTFLHSLGLIEY 130
Db 140 IIPQAPLHLDDEYLGQARHMLSKVGMWDFIDFLDLRLTNGSLVSLTFLHSLGLIEY 199

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QY 131 FHLDMKLRPLVMTQEDYHSQPNVHVAADVTQAMHCYLKEPKLANSVTPWDILSL 190
Db 200 FKLDMKLRPLVMTQEDYHSQPNVHVAADVTQAMHCYLKEPKLANSVTPWDILSL 259
QY 191 TAAATHDLDHPCVQVQPFLLKTNHLYATLYKNTSVLENHWRSAVGLLRSGFLSHLPLES 250
Db 260 LAAAADVDHPCVQVQPFLLKTNHLYATLYKNTSVLENHWRSAVGLLRSGFLSHLPLES 319
QY 251 ROOMETOIGALITLADISQNEYLSLFRSHLDGRDGLCEDTRHRLVLOMALKKADICNP 310
Db 320 TQDIEQQGLSLATDINRQNEFLRLKAHLNKLRLUEDAQRHFMQLQIALKCADICNP 379
QY 311 CRTWELSKQWSEKVTPEEPHQDIEKXVHLGVSPCLDRHTESIANIQIGFMYLYVEPLFT 370
Db 380 CRINEMSKQWSEKVTPEEPHQDIEKXVHLGVSPCLDRHTESIANIQIGFMYLYVEPLFT 439
QY 371 EWARFS-NTRLQTMGLGHVGLNKAQWKGLOREQSSSEDTAA 411
Db 440 EWAHFTGNSTLSEMLGHLAHNAQWKSLLPRQHSRGSSGS 481

RESULT 9
US-09-764-898-280
; Sequence 280, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 280
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (198)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-280

Query Match 48.1%; Score 1079; DB 9; Length 211;
Best Local Similarity 98.1%; Pred. No. 4.7e-104; Indels 0; Gaps 0;
Matches 202; Conservative 1; Mismatches 3;

QY 159 VHAADVQAMHCYLKEPKLANSVTPWDILSLIAAATHDHPGVNQPFLLKTNHLYATL 218
Db 2 IHAADVQAMHCYLKEPKLANSVTPWDILSLIAAATHDHPGVNQPFLLKTNHLYATL 61
QY 219 YKNTSVLENHWRSAVGLLRSGFLSHLPLESQMQETOIGALITLADISQNEYLSLFR 278
Db 62 YKNTSVLENHWRSAVGLLRSGFLSHLPLESQMQETOIGALITLADISQNEYLSLFR 121
QY 279 SHLDGRDGLCEDTRHRLVLOMALKKADICNPRTWELSKQWSEKVTPEEPHQDIEKXV 338
Db 122 SHLDGRDGLCEDTRHRLVLOMALKKADICNPRTWELSKQWSEKVTPEEPHQDIEKXV 181
QY 339 HLGVSPLCDRHTESIANIQIGFMYLY 364
Db 182 HLGVSPLCDRHTESIANIQIGFMYLY 207

RESULT 10
US-09-989-442-120
; Sequence 120, Application US/09989442
; Publication No. US20030013649A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P208
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; CURRENT APPLICATION NUMBER: US/09/989,442
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
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; PRIOR APPLICATION NUMBER: 60/235,834
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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
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; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/229,345
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/229,287
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/229,513
 ; PRIOR FILING DATE: 2000-09-05
 ; PRIOR APPLICATION NUMBER: 60/231,413
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/229,509
 ; PRIOR FILING DATE: 2000-09-05
 ; PRIOR APPLICATION NUMBER: 60/236,367
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/237,039
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/237,038
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/236,370
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/236,802
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/237,037
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 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/240,960
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/239,935
 ; PRIOR FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: 60/239,937
 ; PRIOR FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: 60/241,787
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/246,474
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 ; PRIOR FILING DATE: 2000-08-22
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 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/227,182
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/225,214
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/235,836
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/230,438
 ; PRIOR FILING DATE: 2000-09-06
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 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: 60/225,266
 ; PRIOR FILING DATE: 2000-08-14
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 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/232,080
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/231,414
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/231,244
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/233,064
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 ; PRIOR FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: 60/231,243
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/233,065
 ; PRIOR FILING DATE: 2000-09-14

Query Match 48.1%; Score 1079; DB 10; Length 211;
 Best Local Similarity 98.1%; Pred. No. 4.7e-104;
 Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 159 VHADVTOAMHCYLKBPPLANSVTPDWLILSLIAAATHDLDPGVNQPPFLIKTNHYLATL 218
 :|||||
 Db 2 IHAADVTOAMHCYLKBPPLANSVTPDWLILSLIAAATHDLDPGVNQPPFLIKTNHYLATL 61
 :|||||
 Qy 219 YKNTSVLENHHWSAVGLLRRESGLFSLPLESRQOMETOIGALILATDISRQNEYLSLFR 278
 :|||||
 Db 62 YKNTSVLENHHWSAVGLLRRESGLFSLPLESRQOMETOIGALILATDISRQNEYLSLFR 121
 :|||||
 Qy 279 SHLDGRDCLCLEDTRHRLVLOMALKCADI CNPRTWELSKQWSEKVTTEFFHQGDIEKKY 338
 :|||||
 Db 122 SHLDGRDCLCLEDTRHRLVLOMALKCADI CNPRTWELSKQWSEKVTTEFFHQGDIEKKY 181
 :|||||
 Qy 339 HLGVSPLCDRHTESIANIQIGFMYTL 364
 :|||||
 Db 182 HLGVSPLCDRHTESIANIQIGFMYTL 207
 :|||||

RESULT 11
 US-10-386-414-6
 ; Sequence 6, Application US/10386414

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; Publication No. US20040006016A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; FILE REFERENCE: 55092 AND 10218 MOLECULES AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/10/386,414
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/833,082
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-386-414-6

Query Match      38.8%; Score 871; DB 15; Length 320;
Best Local Similarity 66.9%; Pred. No. 4.7e-82;
Matches 160; Conservative 34; Mismatches 45; Indels 0; Gaps 0;

QY 11 GGVVRVRAGFESRRGSHPIYIDFRIFHSQSEIEVSARNIRRLLSFQYLRSSRFFRG 70
DB 80 GDRLRGQTGVRAERRGSYFFIDFRLNLTSTYSGEIGTKKKVKRLLSFQYFHASRLRG 139
QY 71 TAVNSLNLDDYNGQAKMIEKVGNNWDFLFDRLTNGSLVSLTFLHSLHGLIEY 130
DB 140 IIPQAPLHLLDEYLGQARHMLSKVGWDFLFDRLTNGSLVSLTFLHSLHGLIEH 199
QY 131 FHLDMMLRRFLVMIQEDVHSQMPYHNAHAAVDTQAMCYLKEPKLANSVTPWDILLSL 190
DB 200 FKLDMVTLHRRFLVWVEDVHSQMPYHNAHAAVDTQAMCYLKEPKLANSFLPDLIMGL 259
QY 191 IAAATHDHPGVNQPFLLKTNHYLATLYKNTSVLENHWRSAVGLLRSGFLSHLPLE 249
DB 260 LAAAHADVDPGVNQPFLLKTNHNLANTYQNMVSLVLENHWRSTIGMLRESRLAHLPE 318

RESULT 12
US-10-272-970-17
; Sequence 17, Application US/10272970
; Publication No. US20030139578A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Coleman, Roger T.
```

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; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Fisher, Douglas A.
; TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING PDB8A and PDB8B
; FILE REFERENCE: PC-0054 CIP
; CURRENT APPLICATION NUMBER: US/10/272,970
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 09/454,060
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 09/255,748
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 08/974,565
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: 08/624,663
; PRIOR FILING DATE: 1996-03-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20030139578A1 gi1705952
US-10-272-970-17

Query Match      24.7%; Score 555; DB 14; Length 610;
Best Local Similarity 32.6%; Pred. No. 1.3e-48;
Matches 127; Conservative 77; Mismatches 154; Indels 32; Gaps 7;

QY 8 RMLGDIVRVRAGFESRRGSHPIYIDFRIFHSQSEIEVSARNIRRLLSFQYLRSSRFFRG 63
DB 29 RELTHLSEMSRSGNQVSEVISNTFLD-----KQNEVEIPTSPTPRQ---AFQOPPPSVLR 80
QY 64 SSR-----FFGTAVNSLNI-----LDDYNGQAKMIEKVGNNWDFLFDRLTNG 111
DB 81 QSQPMSQITGLKGLVHTGSLNTNVPFGVKTQDQDLAQLLENLKSGLNIFCVSEYAGG 140
QY 112 NSLVSLLTFLHSLHGLIEYFHLDMMLRRFLVMIQEDVHSQMPYHNAHAAVDTQAMHCY 171
DB 141 RSLSCIMYTIQFQERDLKKFHPVDTMMYMLTLEDHADVAYHNSLHAAADVLSQTHVL 200
QY 172 LKEPKLANSVTPWDILLSLIAAATHDHPGVNQPFLLKTNHYLATLYKNTSVLENHWR 231
DB 201 LATPALDAVFTDLEILAAALFAAAIHVDVDPGVSNQFLINTNSELALMYNDESVLENHHLA 260
QY 232 SAVGLLRSG--LFSHLPLESRQMQETQIGALILATIDSRQNEYLSPFSLHD-----R 283
DB 261 VGFKLQENCDIFQNLKSRQSRQSRKQVMDVMTATDMSKHWMTLLADLKMTVETKKVTS 320
QY 284 GDLCLDETFRHRLVLMQALKACADICNPCKRTWELSKQSEKVTPEFFHQGDIEKKYHLGVS 343
DB 321 GVLLLDNYSDRIQVLRNMVHCADLSNPTKPLELYRQWTDRIWAERFFQGDREGRGMEIS 380
QY 344 PLCDRHRTESIANIQGMFTYLVPELFTWA 373
DB 381 PMCDKHATASVEKSGVGFIDYIVHPLWETWA 410

RESULT 13
US-10-627-929-9
; Sequence 9, Application US/10627929
; Publication No. US20040018605A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice; Cocks, Benjamin G.
; APPLICANT: Coleman, Roger; Seilhamer, Jeffrey J.
; APPLICANT: Fisher, Douglas A.
; TITLE OF INVENTION: CYCLIC NUCLEOTIDE PHOSPHODIESTERASES
; FILE REFERENCE: PF-0057-4 CON
; CURRENT APPLICATION NUMBER: US/10/627,929
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 09/454,060
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 08/974,565
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; PRIOR FILING DATE: 1997-11-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040018605A1 g1705952
US-10-627-929-9

Query Match      24.7%; Score 555; DB 15; Length 610;
Best Local Similarity 32.6%; Pred. No. 1.3e-48;
Matches 127; Conservative 77; Mismatches 154; Indels 32; Gaps 7;

QY 8 RMLGDVVRVRAGFESERRGSHPIYDFRIFHSQSEIEVSVSARNIRLLSFQR-----YLR 63
Db 29 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTROR---AFQPPPSVLR 80
QY 64 SSR-----FFRGTAVSNSLNI-----LDDYNGQAKCMLEKVGWNNPDIPLFDRLTNG 111
Db 81 OSQPMQSLTGLKLVHTGSLNTVNPREGVKTQDQEDLLAQELNSLKWGLNIFCVSEYAGG 140
QY 112 NSLVLTFLPLSLHGLIEYFHLDMKMLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCY 171
Db 141 RSLSCMYTIFQERDLLKHPVDVTMMYMTLTLEDHYHADVAHNSLHAADVLQSTHVL 200
QY 172 LKPKLANSTVPDWILLSLAAATHDLDPGVNQPFLLKTNHYLATLYKNTSVLENHWR 231
Db 201 LAPALDAVFTLEILAAIFAAAIHVDVHPGVSNQFLINTNSELALMYNDESLENHHLA 260
QY 232 SAVGLLRRESG--LFSHLPLESQQMETQIGALIIATDISRQNEVLSLFRSHLD-----R 283
Db 261 VGFKLQEEKNCDFQNLSEKQSRQSLKQVDMVLTADMSKHTLLADLKTWETKVTSS 320
QY 284 GDLCLEDRHRHLVLQALMKAICINPCRTWELSKQWSEKVTBEFFHQGDIEKKYHLGVS 343
Db 321 GVLLLDNYSRIQVLRNMVHCADLSNPTKSLLEYRQWTDRIEAEFFQGGDKERERGMWIS 380
QY 344 PLCDRHTESANIQIGPMYTLVEPLPTEWA 373
Db 381 PMCDKHTASVEKSGVGFIDYIVHPLWETWA 410

RESULT 14
US-09-983-754-2
; Sequence 2, Application US/09983754
; Publication No. US20030084374A1
; GENERAL INFORMATION:
; APPLICANT: EXONHIT THERAPEUTICS SA
; APPLICANT: AIT IKHLEF, ali
; APPLICANT: RESINK, Annelies
; APPLICANT: SCHWEIGHOFFER, Fabien
; TITLE OF INVENTION: Molecular Target of Neurotoxicity
; FILE REFERENCE: B0100US
; CURRENT APPLICATION NUMBER: US/09/983,754
; CURRENT FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 721
; TYPE: PRT
; ORGANISM: souris
US-09-983-754-2

Query Match      24.6%; Score 551; DB 12; Length 721;
Best Local Similarity 31.8%; Pred. No. 4.3e-48;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

QY 8 RMLGDVVRVRAGFESERRGSHPIYDFRIFHSQSEIEVSVSARNIR-----LLSF 58
Db 241 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTROR-----LLSF 295

RESULT 15
US-10-442-675-2
; Sequence 2, Application US/10442675
; Publication No. US20040086900A1
; GENERAL INFORMATION:
; APPLICANT: Wigler, M.
; APPLICANT: Colicelli, J.
; TITLE OF INVENTION: Method for Identifying Modulators Gene Expression
; FILE REFERENCE: 27866/39366
; CURRENT APPLICATION NUMBER: US/10/442,675
; CURRENT FILING DATE: 2003-05-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-442-675-2

Query Match      24.5%; Score 550; DB 16; Length 517;
Best Local Similarity 31.8%; Pred. No. 3.4e-48;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

QY 8 RMLGDVVRVRAGFESERRGSHPIYDFRIFHSQSEIEVSVSARNIR-----LLSF 58
Db 37 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTROR-----LLSF 91
QY 59 QYLRSSRFRGTAVSN-SINILDDYNGQAKCMLEKVGWNNPDIPLFDRLTNGSLVSL 117
Db 92 VKKLMHSSSLNNTSISIRFGVNTENEDHLAKE---LEDLKNKGLNIFNVAGYSNRELTCTI 148
QY 118 TPHLSLHGLIEYFHLDMKMLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYKPKL 177
Db 149 MYAIFQERDLLKTKFISSDTFTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLSTPAL 208
QY 178 ANSVTPWDILLSLIAAATHDLDPGVNQPFLLKTNHYLATLYKNTSVLENHWRSAVGLL 237
Db 209 DAVFTOLEILAAIFAAAIHVDVHPGVSNQFLINTNSELALMYNDESLENHHLAVGFKLL 268
QY 238 RES--GLFSHLPLESQQMETQIGALIIATDISRQNEVLSLFRSHLD-----RGDLCLE 289
Db 269 QEEHCDIFQNLTKKQRTLRKMWIDMLATDMSKMSLLADLKTWETKVTSSGVLLLD 328
QY 290 DTRHRHLVLQALMKAICINPCRTWELSKQWSEKVTBEFFHQGDIEKKYHLGVSPLCDRH 349
Db 329 NYTDRIQVLRNMVHCADLSNPTKSLLEYRQWTDRIEAEFFQGGDKERERGMWISPCDKH 388

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Oy 350 TESIANIOIGFMTYLVLEPLTEWA 373
Db 389 TASVEKSQVGFIDYVHPLWETWA 412

Search completed: May 26, 2004, 09:42:42
Job time : 578 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2004, 09:24:28 ; Search time 21 Seconds
(without alignments)
1951.314 Million cell updates/sec

Title: US-09-966-781A-1
Perfect score: 2243
Sequence: 1 DQALYIRMLGVDVRSRAG.....DTDAAFELNSQLLPQENRLS 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2243	100.0	438	A47286	3',5'-cyclic-AMP p
2	1403.5	62.6	450	JC7466	3',5'-cyclic-nucle
3	555	24.7	610	I67946	3',5'-cyclic-nucle
4	555	24.7	844	I53865	phosphodiesterase
5	550	24.5	562	I59143	cAMP phosphodiesterase
6	550	24.5	564	JC1519	3',5'-cyclic-nucle
7	550	24.5	564	A40949	cyclic-AMP phospho
8	550	24.5	736	I61354	phosphodiesterase
9	542	24.2	673	I61358	3',5'-cyclic-nucle
10	541	24.1	886	A54442	3',5'-cyclic-nucle
11	539	24.0	584	B53109	3',5'-cyclic-nucle
12	539	24.0	584	I61259	3',5'-cyclic-nucle
13	536	23.9	712	S71626	3',5'-cyclic-nucle
14	534.5	23.8	536	I67945	3',5'-cyclic-nucle
15	503	22.4	713	JW0088	3',5'-cyclic-nucle
16	493.5	22.0	549	T16769	hypothetical prote
17	489	21.8	323	S55348	3',5'-cyclic-nucle
18	482	21.5	664	T24459	hypothetical prote
19	478.5	21.3	777	S65543	3',5'-cyclic-nucle
20	471.5	21.0	659	JE0293	3',5'-cyclic-nucle
21	471.5	21.0	885	JC7898	3',5'-cyclic-nucle
22	470.5	21.0	534	A44162	3',5'-cyclic-nucle
23	470.5	21.0	535	A46378	3',5'-cyclic-nucle
24	470	21.0	267	B33904	cAMP phosphodiesterase
25	469.5	20.9	535	A44161	3',5'-cyclic-nucle
26	461	20.6	768	T10796	3',5'-cyclic-nucle
27	457.5	20.4	536	JC6129	3',5'-cyclic-nucle
28	452	20.2	519	T14783	hypothetical prote
29	439.5	19.6	530	A45334	3',5'-cyclic-nucle

ALIGNMENTS

RESULT 1

A47286
3',5'-cyclic-AMP phosphodiesterase (EC 3.1.4.-) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 03-Nov-2000
C:Accession: A47286
R:Michaeli, T.; Bloom, T.J.; Martins, T.; Loughney, K.; Ferguson, K.; Riggs, M.; Rodge:
J. Biol. Chem. 268, 12925-12932, 1993
A:Title: Isolation and characterization of a previously undetected human cAMP phosphod:
C:Reference number: A47286; MUID:93286141; PMID:8389765
A:Accession: A47286
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-498 <MIC>
A:Cross-references: GB:I12052; NID:G179892; PID:G179893
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',
C:Keywords: phosphoric diester hydrolase
F:227-447/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 100.0%; Score 2243; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 6.2e-177;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DOTALYIRMLGVDVRSRAGFSEERGSHPYIDFRIFHSQSEIEVSVAARNIRLLISFOR	60
DB	73	DQALYIRMLGVDVRSRAGFSEERGSHPYIDFRIFHSQSEIEVSVAARNIRLLISFOR	132
QY	61	YLRSSFFRGTAVSNSLNILDDYNGQAKCMLEKVGNNWDFLFDRLTNGSLVSLTFH	120
DB	133	YLRSSFFRGTAVSNSLNILDDYNGQAKCMLEKVGNNWDFLFDRLTNGSLVSLTFH	192
QY	121	LPSLGLIIEYFHLDMKLRRLVMIQEDYHSQNPYHNAVAADVTQAMHCYLKEPKLANS	180
DB	193	LFSLGLIIEYFHLDMKLRRLVMIQEDYHSQNPYHNAVAADVTQAMHCYLKEPKLANS	252
QY	181	VPWDILLSLIAAATHDLHPGVNQPFLLKTNHYLATLYKNTSVLENHHRWSAVGLLRES	240
DB	253	VPWDILLSLIAAATHDLHPGVNQPFLLKTNHYLATLYKNTSVLENHHRWSAVGLLRES	312
QY	241	GLFSLPLESRQOMETQIGALILATDISRQNEVLSLFRSHLDKGLDCLDTRRHVLQW	300
DB	313	GLFSLPLESRQOMETQIGALILATDISRQNEVLSLFRSHLDKGLDCLDTRRHVLQW	372
QY	301	ALKACDINCPRTWELSKQSEKVTPEFPHQGDIEKKYHLGVSPICDRHTESIANIQIGF	360
DB	373	ALKACDINCPRTWELSKQSEKVTPEFPHQGDIEKKYHLGVSPICDRHTESIANIQIGF	432
QY	361	MTYLVPELTFEAFSNTLSQTMGLGHVGNKASWKGLOEQSSSEDTEAAFEINSQLLP	420
DB	433	MTYLVPELTFEAFSNTLSQTMGLGHVGNKASWKGLOEQSSSEDTEAAFEINSQLLP	492
QY	421	QENRLS	426

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-844 <RES>
A:Cross-references: GB:L27057; NID:G3334904; PIDN:AAC27098.1; PID:G436004
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology
F:418-646/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.7%; Score 555; DB 2; Length 844;
Best Local Similarity 32.6%; Pred. No. 1.7e-37;
Matches 127; Conservative 77; Mismatches 154; Indels 32; Gaps 7;

QY 8 RMLGDVVRVRAGSEERRGSHPYIDFRIFHSQSIEVSVSARNIR 7
DB 263 RELTHLSMSRSGNQVSEYISNTFLD-----KQNEVIPSPTQR---AFQPPPSVLR 314
QY 64 SSR-----PFRGTVANSUNI-----LDDYNGQAKCMLEKGVNNFNDFLDRITNG 111
DB 315 QSQPMSQITGLKLVHTGSLNTNVRFGVKTQDQLLAQALENLSKWLGNIFCVSEYAGG 374
QY 112 NSLVSLTFHLSHGLIEYFLDMKMLRFLVLMQEDYHSQNPYHNAHADVTQAMHCY 171
DB 375 RSLSCIMTYIPQERDLKKFHIPVDTMMYMLTLEDHYHADVYHNSLHAADVLQSTHVL 434
QY 172 LKPEPLANSVTPWDILLSLIAAAATHDLHPGVNQPFELIKTHYLATLYKNTSVLENHHR 231
DB 435 LATPALDAVFTDLELAALFAAAHDVDHPGVSNQFLINTNSALMYNDESVLNHHLA 494
QY 232 SAVGLLRSG--LPSHLPESRQMETQIGALIIATDISRQNEVLSLFRSHLD-----R 283
DB 495 VGFGLQEBNCIDIFQNLKSRQSLRKQVDMVLDATDMSKHTLLADLKTMTVKVTS 554
QY 284 GDLCLDTRHRLHVLQWALKCADICNCPRTWELSKQWSEKVTREFFHQGDIEKKYHLGVS 343
DB 555 GVLLDNVSDRIQVRNWHCADLSNPKYPLRQWTDRIAMAFPOQDRERGRGMEIS 614
QY 344 PLCDRHTSTIANIQIGFMTYLVPELFTWA 373
DB 615 PMCDKHTASVEKSQVGFIDYIVHPLMETWA 644

RESULT 5
I59143
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 03-Nov-2000
C:Accession: I59143
R:Colicelli, J.; Birchmeier, C.; Michaeli, T.; O'Neill, K.; Riggs, M.; Wiegler, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 3599-3603, 1989
A:Title: Isolation and characterization of a mammalian gene encoding a high-affinity cAMP phosphodiesterase
A:Reference number: I59143; MUID:89264471; PMID:2542941
A:Accession: I59143
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-562 <RES>
A:Cross-references: GB:J04563; NID:G203967; PIDN:AAA66039.1; PID:G203968
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
F:231-459/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.5%; Score 550; DB 2; Length 562;
Best Local Similarity 31.8%; Pred. No. 2.5e-37;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

QY 8 RMLGDVVRVRAGSEERRGSHPYIDFRIFHSQSIEVSVSARNIR 58
DB 82 RELTHLSMSRSGNQVSEYISNTFLD-----KQNDVEIPSPQDKREKKKKQQLMTQISG 136
QY 59 QRYLRSSRFRFGTVASN--SLNILDYNGQAKCMLEKGVNNFNDFLDRITNGNSVLSL 117
DB 137 VKLMSHSSSLNTSISRGVNTENEDHLAKE---LEDLNKWLGNIFNVAGVSHRPLTCI 193
QY 118 TFHLSHGLIEYFLDMKMLRFLVLMQEDYHSQNPYHNAHADVTQAMHCYKPKL 177
DB 194 MYAIFQERDLKTFKISSDTFTVYMWTLDEHYSDVAYHNSLHAADVAQSTHVLSTPAL 253

QY 178 ANSVTPWDILLSLIAAATHDLHPGVNQPFELIKTHYLATLYKNTSVLENHHRSAVGLL 237
DB 254 DAVFTDLEIIAALFAAAHVDHPGVSNQFLINTNSALMYNDESVLNHHLAVGFKL 313
QY 238 RES--GLFSLHPLESRQMETQIGALIIATDISRQNEVLSLFRSHLD-----RGDLCLC 289
DB 314 QEEHCDIFQNLTKQRTLRKWDVMDVLDATDMSKMSILLADLKTMTVKVTSVSSVGLLDD 373
QY 290 DTRHRLHVLQWALKCADICNCPRTWELSKQWSEKVTREFFHQGDIEKKYHLGVSPLCDRH 349
DB 374 NYTDRIQVLRNWHCADLSNPKYPLRQWTDRIAMEEFFQQDKERGRGMEISPMCDKH 433
QY 350 TESTANTQIGFMTYLVPELFTWA 373
DB 434 TASVEKSQVGFIDYIVHPLMETWA 457

RESULT 6
JC1519
C:Species: Homo sapiens (man)
C>Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 21-Jul-2000
C:Accession: JC1519; A45500; I61359
R:Oberholte, R.; Bhakta, S.; Alvarez, R.; Bach, C.; Zuppan, P.; Mulkins, M.; Jarnagin, Gene 129, 239-247, 1993
A:Title: The cDNA of a human lymphocyte cyclic-NMP phosphodiesterase (PDE IV) reveals a
A:Reference number: JC1519; MUID:93314968; PMID:8392015
A:Accession: JC1519
A:Molecule type: mRNA
A:Residues: 1-564 <OBE>
A:Cross-references: GB:L12686
A:Experimental source: lymphocyte
A>Note: only partial nucleotide sequence is given
R:McLaughlin, M.M.; Cieslinski, L.B.; Burman, M.; Torphy, T.J.; Livi, G.P.
J. Biol. Chem. 268, 6470-6476, 1993
A:Title: A low-Km, rolipram-sensitive, cAMP-specific phosphodiesterase from human brain
f mRNA
A:Reference number: A45500; MUID:93203241; PMID:8384210
A:Accession: A45500
A:Molecule type: mRNA
A:Residues: 1-564 <MCL>
A:Cross-references: GB:M97515; NID:G292387; PIDN:AAA36426.1; PID:G292388
A:Experimental source: frontal cortex
A>Note: sequence extracted from NCBI backbone (NCBIN:127929, NCBI:P:127930)
R:Polger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, Mol. Cell. Biol. 13, 6558-6571, 1993
A:Title: A family of human phosphodiesterases homologous to the dunce learning and memc
A:Reference number: A54442; MUID:94019330; PMID:8413254
A:Accession: I61359
A>Status: preliminary; nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-564 <RES>
A:Cross-references: GB:L20971; NID:G347131; PIDN:AAA03593.1; PID:G347132
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
C:Keywords: phosphoric diester hydrolase
F:233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.5%; Score 550; DB 2; Length 564;
Best Local Similarity 31.8%; Pred. No. 2.5e-37;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

QY 8 RMLGDVVRVRAGSEERRGSHPYIDFRIFHSQSIEVSVSARNIR 58
DB 84 RELTHLSMSRSGNQVSEYISNTFLD-----KQNDVEIPSPQDKREKKKKQQLMTQISG 138
QY 59 QRYLRSSRFRFGTVASN--SLNILDYNGQAKCMLEKGVNNFNDFLDRITNGNSVLSL 117
DB 139 VKLMSHSSSLNTSISRGVNTENEDHLAKE---LEDLNKWLGNIFNVAGVSHRPLTCI 195
QY 118 TFHLSHGLIEYFLDMKMLRFLVLMQEDYHSQNPYHNAHADVTQAMHCYKPKL 177
DB 196 MYAIFQERDLKTFKISSDTFTVYMWTLDEHYSDVAYHNSLHAADVAQSTHVLSTPAL 255

QY 178 ANSVTPWDILLSLIAAATHDLDPGVNQPLIKTNHYLATLYKNTSVLENHHWRSVGLL 237
 Db 256 DAVFTDLEILAAIAFAAAIHVDHPGVSNQFLINTNSGALMYNDESVLENHHLAVGFKLL 315
 QY 238 RES--GLFSLPLPESQOMETQIGALILATDISRQNEYLSLFRSHLD-----RGDLCL 289
 Db 316 QEEHCDFMNLTKKQQTLRKQVDMVLAIDMSKMSLLADLTKMTVETKVTSSGVLDD 375
 QY 290 DTRHRLVLMALKCADI CNPCRTWELSKQWSEKVTPEEFHQGDIEKKYHLGVSPICDRH 349
 Db 376 NYTDRIQVLRNMVHCADLSNPTKSLLEYLRQWTDRIEETFFQGDKERERGMESPWCCKH 435
 QY 350 TESIANIQGFMTYLYVEPLFEWA 373
 Db 436 TASVEKSGVGFIDYIVHPLMETWA 459

RESULT 7
 A40949
 cyclic-AMP phosphodiesterase (EC 3.1.4.-) - rat
 N/Alternate names: PDE4/IVb long form
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 13-May-1992 #sequence revision 13-May-1992 #text_change 09-Jun-2000
 C/Accession: A40949; D33904; A53109; I67942
 R/Swinnen, J.V.; Tsikalas, K.E.; Conti, M.
 J. Biol. Chem. 266, 18370-18377, 1991
 A/Title: Properties and hormonal regulation of two structurally related cAMP phosphodies
 A/Reference number: A40949; MUID:92011578; PMID:1655746
 A/Accession: A40949
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-564 <SWI>
 A/Cross-references: GB:M25350
 R/Swinnen, J.V.; Joseph, D.R.; Conti, M.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989
 A/Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP P
 A/Reference number: A33904; MUID:89315790; PMID:2546153
 A/Accession: D33904
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 210-476 <SW2>
 A/Cross-references: GB:M25350
 R/Monaco, L.; Vicini, E.; Conti, M.
 J. Biol. Chem. 269, 347-357, 1994
 A/Title: Structure of two rat genes coding for closely related rolipram-sensitive cAMP P
 A/Reference number: A53109; MUID:94103234; PMID:8276818
 A/Accession: A53109
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-358, 'S', 360-564 <MON>
 A/Cross-references: GB:U01291; NID:G409826; PIDN:AAA18926.1; PID:G409828
 R/Bolger, G.B.; Rodgers, L.K.; Riggs, M.
 Gene 149, 237-244, 1994
 A/Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
 A/Reference number: I53865; MUID:95047483; PMID:7958996
 A/Accession: I67942
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-564 <RES>
 A/Cross-references: GB:L27058; NID:G950096; PIDN:AAA74478.1; PID:G598375
 C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
 C/Keywords: alternative initiators; alternative splicing; phosphoric diester hydrolase
 F;233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.5%; Score 550; DB 2; Length 564;
 Best Local Similarity 31.8%; Pred. No. 2.5e-37;
 Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

QY 8 RMLGDVVRVRAGFESERRGSHPIYDFRIFHSQSEIEVSVSARNIRR-----LLSF 58
 Db 84 RELTHLSEMSRSGNVSEYISNTFLD-----KQNDVEIPSTQKREKKKQQLMTQISG 138

QY 59 QRYLSSRRFRGTAVSN-SLNLDDYNGQAKCMLEKGVGNWPFDFLFDRLTNGSLVSL 117
 Db 139 VKKLMHSSSLNNTSISRFVNTENEDHLAKE---LEDLNKWLNIENFVAGYSHNRPLTCTI 195
 QY 118 TFLHLSLHGLIEFHLDMKLRFRFVMIQEDYHSQNPYHNAAADVTQAMHCYKPEKL 177
 Db 196 MYAIFQERDLLTKFRISSDTFITYMTLEDHVSVDVYHNSLHAADVAQSTHVLSTPAL 255
 QY 178 ANSVTPWDILLSLIAAATHDLDPGVNQPLIKTNHYLATLYKNTSVLENHHWRSVGLL 237
 Db 256 DAVFTDLEILAAIAFAAAIHVDHPGVSNQFLINTNSGALMYNDESVLENHHLAVGFKLL 315
 QY 238 RES--GLFSLPLPESQOMETQIGALILATDISRQNEYLSLFRSHLD-----RGDLCL 289
 Db 316 QEEHCDFMNLTKKQQTLRKQVDMVLAIDMSKMSLLADLTKMTVETKVTSSGVLDD 375
 QY 290 DTRHRLVLMALKCADI CNPCRTWELSKQWSEKVTPEEFHQGDIEKKYHLGVSPICDRH 349
 Db 376 NYTDRIQVLRNMVHCADLSNPTKSLLEYLRQWTDRIEETFFQGDKERERGMESPWCCKH 435
 QY 350 TESIANIQGFMTYLYVEPLFEWA 373
 Db 436 TASVEKSGVGFIDYIVHPLMETWA 459

RESULT 8
 I61354
 phosphodiesterase - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Sep-1996 #sequence revision 06-Sep-1996 #text_change 17-Nov-2000
 C/Accession: I61354
 R/Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
 Mol. Cell. Biol. 13, 6558-6571, 1993
 A/Title: A family of human phosphodiesterases homologous to the dunce learning and mem
 A/Reference number: A54442; MUID:94019330; PMID:8413254
 A/Accession: I61354
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-736 <RES>
 A/Cross-references: GB:I20966; NID:G347121; PIDN:AAA03589.1; PID:G347122
 C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
 F;405-633/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.5%; Score 550; DB 2; Length 736;
 Best Local Similarity 31.8%; Pred. No. 3.7e-37;
 Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

QY 8 RMLGDVVRVRAGFESERRGSHPIYDFRIFHSQSEIEVSVSARNIRR-----LLSF 58
 Db 256 RELTHLSEMSRSGNVSEYISNTFLD-----KQNDVEIPSTQKREKKKQQLMTQISG 310

QY 59 QRYLSSRRFRGTAVSN-SLNLDDYNGQAKCMLEKGVGNWPFDFLFDRLTNGSLVSL 117
 Db 311 VKKLMHSSSLNNTSISRFVNTENEDHLAKE---LEDLNKWLNIENFVAGYSHNRPLTCTI 367
 QY 118 TFLHLSLHGLIEFHLDMKLRFRFVMIQEDYHSQNPYHNAAADVTQAMHCYKPEKL 177
 Db 368 MYAIFQERDLLTKFRISSDTFITYMTLEDHVSVDVYHNSLHAADVAQSTHVLSTPAL 427
 QY 178 ANSVTPWDILLSLIAAATHDLDPGVNQPLIKTNHYLATLYKNTSVLENHHWRSVGLL 237
 Db 428 DAVFTDLEILAAIAFAAAIHVDHPGVSNQFLINTNSGALMYNDESVLENHHLAVGFKLL 487
 QY 238 RES--GLFSLPLPESQOMETQIGALILATDISRQNEYLSLFRSHLD-----RGDLCL 289
 Db 488 QEEHCDFMNLTKKQQTLRKQVDMVLAIDMSKMSLLADLTKMTVETKVTSSGVLDD 547
 QY 290 DTRHRLVLMALKCADI CNPCRTWELSKQWSEKVTPEEFHQGDIEKKYHLGVSPICDRH 349
 Db 548 NYTDRIQVLRNMVHCADLSNPTKSLLEYLRQWTDRIEETFFQGDKERERGMESPWCCKH 607
 QY 350 TESIANIQGFMTYLYVEPLFEWA 373

Db 608 TASVEKSOVGFIDYIVHPLWETWA 631

RESULT 9

I61358

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific - human

N:Alternate names: 3',5'-cyclic-AMP phosphodiesterase, rolipram-sensitive

C:Species: Homo sapiens (man)

C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 17-Nov-2000

C:Accession: I61358; I38416

R:Polger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, Mol. Cell. Biol. 13, 6558-6571, 1993

A:Title: A family of human phosphodiesterases homologous to the dunce learning and memory

A:Reference number: A54442; MUID:94019330; PMID:8413254

A:Accession: I61358

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-673 <RES>

A:Cross-references: GB:L20970; NID:G347129; PIDN:AAA03592.1; PID:G347130

R:Baeker, P.A.; Oernolte, R.; Bach, C.; Yee, C.; Shelton, E.R.

Gene 138, 253-256, 1994

A:Title: Isolation of a cDNA encoding a human rolipram-sensitive cyclic AMP phosphodiesterase

A:Reference number: I38416; MUID:94171048; PMID:8125310

A:Accession: I38416

A:Molecule type: mRNA

A:Residues: 70-507, 'P', 509-673 <RE2>

A:Cross-references: EMBL:U02882; NID:G433346; PIDN:AAC13745.1; PID:G433347

C:Genetics:

A:Gene: GDB:PDE4D; DPDE3

A:Cross-references: GDB:132541; OMIM:600129

A:Map position: 5q12-5q12

C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'

C:Keywords: cAMP binding; phosphoric diester hydrolase

F:325-553/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 24.2%; Score 542; DB 2; Length 673;

Best Local Similarity 31.6%; Pred. No. 1.5e-36;

Matches 122; Conservative 82; Mismatches 150; Indels 32; Gaps 7;

QY 8 RMLGVRVRSRAGFSESRGSHPYDFRIFHSQSIEV-----SVSARNIRLLSFQ 59

Db 178 RELTHLSMSRSGNQVSEFISNTFLD-----KQHEVEIPSPQKEKKRPMSSQISGVK 232

QY 60 RYLRSRRFRGFAVNS---LNILDDYNGQAKCMLEKVGNNWFDFLFDLTNGNSLV 115

Db 233 KLMHSS-----SLNSSIPRGVKTQEDVLAK-ELEDVKNKGLHVFRIALSGNRPLT 285

QY 116 SLTFHLSLGLIEYFHLDMKLRPLVMIOEDYHSQNPYHNAVHAADVTQAMHCYLKEP 175

Db 286 VIMHTIFQRDLTKFKIPVDLTLYLTLEDDYHADVAHNNIHAADVQSTHVLSTP 345

QY 176 KLANSVTPWDILSLIAAATHLDHPGVNQPFILIKTNHYLATLYKNTSVLENHHRSAVG 235

Db 346 ALAEVFTDLLEILAAIFAGAIHVDHPGVNSQFLINTNSLALMYNDSSVLENHHLAVGFK 405

QY 236 LIRESG--LFSHLPESRQOMETQICALILATDISRQNEYLSLFRSHLD-----RGDLIC 287

Db 406 LLQENCDIFQNLTKKQSLRKWIDIVLATDMSKWNLLADLKTWETKVTSSGVLL 465

QY 288 LEDTRHRLVLQMALKCADICNCPRTWELSKQWSEKVTVEFFHQGDIEKKYHLGVSPICD 347

Db 466 LDNYSDRIQVLQNMVHCADLSNPTKPLQYRQWTDRIIMEEFFRQGRERERGMSEI5MCD 525

QY 348 RTEISIANIQIGFMTYVLEPLTEWA 373

Db 526 KENASVEKSOVGFIDYIVHPLWETWA 551

RESULT 10

A54442

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, cAMP-specific, long splice f

N:Contains: 3',5'-cyclic AMP phosphodiesterase HPDE4A6 splice form

C:Species: Homo sapiens (man)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000

C:Accession: A54442; S55788; A36317; S55787

R:Polger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, Mol. Cell. Biol. 13, 6558-6571, 1993

A:Title: A family of human phosphodiesterases homologous to the dunce learning and mem

A:Reference number: A54442; MUID:94019330; PMID:8413254

A:Accession: A54442

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-886 <RES>

A:Cross-references: GB:L20965; NID:G347119; PIDN:AAA03588.1; PID:G347120

R:Sullivan, M.; Egerton, M.; Shakur, Y.; Marguarden, A.; Houslay, M.D.

Cell. Signal. 6, 793-812, 1994

A:Title: Molecular cloning and expression, in both COS-1 cells and S. cerevisiae, of a

A:Reference number: S55788; MUID:95194817; PMID:7888306

A:Accession: S55788

A:Molecule type: mRNA

A:Residues: 'MCPFPVTV', 210-735, 'E', 737-886 <SUL>

A:Cross-references: EMBL:U18087; NID:G604374; PIDN:AAC50458.1; PID:G604375

A:Note: 736-Ala was also found

R:Livi, G.P.; Kmetz, P.; McHale, M.M.; Cieslinski, L.B.; Sathe, G.M.; Taylor, D.P.; Dav

Mol. Cell. Biol. 10, 2678-2686, 1990

A:Title: Cloning and expression of cDNA for a human low-K-m, rolipram-sensitive cyclic

A:Reference number: A36317; MUID:90258854; PMID:2160582

A:Accession: A36317

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 'MCPFPVTV', 210-516, 'Y', 518-722, 'R', 724-726, 'R', 728-735, 'E', 737-788, 'E', 793

C:Genetics:

A:Gene: GDB:PDE4A; DPDE2

A:Cross-references: GDB:138776; OMIM:600126

A:Map position: 19p13.1-19q12

C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology

C:Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase

F:432-660/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.1%; Score 541; DB 2; Length 886;

Best Local Similarity 32.3%; Pred. No. 2.6e-36;

Matches 124; Conservative 69; Mismatches 159; Indels 32; Gaps 6;

QY 22 ESERRGSH--PYDPRIFHSQSIEVSVSARNIRLLSFQR-----YLRSRRF 67

Db 275 EMSRSGNQVSEVISITTFDLKQNEVEIPSPMKEREKQCAPRPPSQPPPPVPHLPQMSQ 334

QY 68 FRGTAV---SNSLN-----LDDYNGQAKCMLEKVGNNWFDFLFDLTNGNSLVL 117

Db 335 ITGLKKLMHSSNLSNNSNIPRFGVKTDQBELLAQELNENKMGILNFCVSDYAGGRSLTCI 394

QY 118 TPLHLSLGLIEYFHLDMKLRRLFMIOEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177

Db 395 MYMIFQERDLKKFKFIPVDVTWYMTLEDYHADVAHNSLHAADVLOSTHVLATPAL 454

QY 178 ANSVTPWDILSLIAAATHLDHPGVNQPFILIKTNHYLATLYKNTSVLENHHRSAVGIL 237

Db 455 DAVFTDLBILAAALFAALHVDHPGVNSQFLINTNSLALMYNDSSVLENHHLAVGFKLL 514

QY 238 RESG--LFSHLPESRQOMETQIGALILATDISRQNEYLSLFRSHLD-----RGDICLE 289

Db 515 QEDNCIDIFQNLTKKQSLRKWIDIVLATDMSKHMTLLADLKTWETKVTSSGVLLD 574

QY 290 DTRHRLVLQMALKCADICNCPRTWELSKQWSEKVTVEFFHQGDIEKKYHLGVSPICDRH 349

Db 575 NYSRIQVLRNMVHCADLSNPTKPLQYRQWTDRIIMAEFFRQGRERERGMSEI5MCDKH 634

QY 350 TESTIANIQIGFMTYVLEPLTEWA 373

Db 635 TASVEKSOVGFIDYIVHPLWETWA 658

RESULT 11

BS3109

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4B, cAMP-specific, splice form

C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Jul-1995 #sequence revision 07-Jul-1995 #text_change 19-May-2000
C:Accession: B53109; A34114; C33904; I67944
J:Monaco, L.; Vicini, E.; Conti, M.
J: Biol. Chem. 269, 347-357, 1994
A:Title: Structure of two rat genes coding for closely related rolipram-sensitive cAMP P
A:Reference number: A53109; MUID:94103234; PMID:8276818
A:Accession: B53109
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-584 <NON>
A:Cross-references: GB:U01280
R:Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 8197-8201, 1989
A:Title: The mRNA encoding a high-affinity cAMP phosphodiesterase is regulated by hormon
A:Reference number: A34414; MUID:90046763; PMID:2554303
A:Accession: A34414
A:Molecule type: mRNA
A:Residues: 1-584 <SWI>
A:Cross-references: GB:U09455; GB:M25349; NID:G517501; PIDN:AAA20401.1; PID:G517502; GB:
R:Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989
A:Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP P
A:Reference number: A33904; MUID:89315790; PMID:2546153
A:Accession: C33904
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 214-480 <SW2>
A:Cross-references: GB:M25349
R:Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A:Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A:Reference number: I53865; MUID:95047482; PMID:7958996
A:Accession: I67944
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'E'FFGES', 34-421, 'E', 423-584 <RES>
A:Superfamily: 3', 5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3', 5'
C:Keywords: 3', 5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3', 5'
F:237-465/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.0%; Score 539; DB 2; Length 584;
Best Local Similarity 31.6%; Pred. No. 2.1e-36;
Matches 122; Conservative 81; Mismatches 151; Indels 32; Gaps 7;

QY 8 RMLGDRVRSRAGFESERRGSHPYIDFRIFHSQSIEV-----SVSARNIRRLISFQ 59
Db 90 RELTHLSEMSRSGNQVSEYISNTFLD-----KQHEVEIPSPQKEKKEKKRPMQSQISGVK 144
QY 60 RYLRSRFRGTAVNS-----LNILDDYNGQAKCMLEKVGNNFDFLDTNGNSLV 115
Db 145 KLMHSS-----SLTNSCIPRFGVKTQEVDLAK-ELEDVKNKGLHVFRIAEISGNRPLT 197
QY 116 SLTFHLFSLHGLIEYFHLDMKRLRFLVMIQEDYHSQNPYHNAVHAADVTOAMHCYLKEP 175
Db 198 VIMHTIFQERDLTKFKIPVDLTITLMTLEDHYADVAHNNIHAADVQSTHVLSTP 257
QY 176 KLANSVTPMDILLSLIAAATHDLDPGVNQPFLLKTNHYLATYKNTSVLENHHRSAVG 235
Db 258 ALAEAVTDLEILAAIFASAIHDVDPGVSNQFLINTNSALMYNDSSVLENHHLAVGFK 317
QY 236 LIRESG--LFSHLPLESRQOMETQIGALILATDISRQNEVLSLFRSHLD-----RGDLC 287
Db 318 LLQENCDIFQNLTKKQSLRKAIDIVLATDMSKHMLLADLTKMTVETKVTSSGVLL 377
QY 288 LEDTRHRLVLMALKACADICNCRTWELSKQWSEKVEFFHQGDIEKKYHLGVSPCLD 347
Db 378 LDNYSRIQVLMNVHCADLSNPTKPLQLYROWTDRIMEEFFRQGRERERGMWISPMCD 437
QY 348 RHETSIANIQIGPMTYVPEPLTEWA 373
Db 438 KINASVEKSOVGFIDYIVHPLWETWA 463

RESULT 12

I61259
3', 5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific, splice form
N:Alternate names: cyclic-AMP phosphodiesterase
N:Contains: 3', 5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific,
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 17-Nov-2000
C:Accession: I61259; A53678; I67943
R:Sette, C.; Vicini, E.; Conti, M.
J. Biol. Chem. 269, 18271-18274, 1994
A:Title: The rat PDE3/IVD phosphodiesterase gene codes for multiple proteins differentia
A:Reference number: A53678; MUID:94308045; PMID:8034568
A:Accession: I61259
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-672 <RES>
A:Cross-references: EMBL:U09457; NID:G517418; PID:G517419
A:Accession: A53678
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 167-672 <RE2>
A:Cross-references: EMBL:U09456; NID:G517416; PIDN:AAA20393.1; PID:G517417
R:Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A:Title: Differential CNS expression of alternative mRNA isoforms of the mammalian gen
A:Reference number: I53865; MUID:95047482; PMID:7958996
A:Accession: I67943
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'N', 96-625, 'Y', 627-672 <RE3>
A:Cross-references: GB:L27059; NID:G436007; PIDN:AAA56857.1; PID:G436008
C:Genetics:
A:Gene: PDE3/IVD gene
C:Superfamily: 3', 5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3', 5'
C:Keywords: cAMP binding; phosphoric diester hydrolase
F:325-553/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.0%; Score 539; DB 2; Length 672;
Best Local Similarity 31.6%; Pred. No. 2.6e-36;
Matches 122; Conservative 81; Mismatches 151; Indels 32; Gaps 7;

QY 8 RMLGDRVRSRAGFESERRGSHPYIDFRIFHSQSIEV-----SVSARNIRRLISFQ 59
Db 178 RELTHLSEMSRSGNQVSEYISNTFLD-----KQHEVEIPSPQKEKKEKKRPMQSQISGVK 232
QY 60 RYLRSRFRGTAVNS-----LNILDDYNGQAKCMLEKVGNNFDFLDTNGNSLV 115
Db 233 KLMHSS-----SLTNSCIPRFGVKTQEVDLAK-ELEDVKNKGLHVFRIAEISGNRPLT 285
QY 116 SLTFHLFSLHGLIEYFHLDMKRLRFLVMIQEDYHSQNPYHNAVHAADVTOAMHCYLKEP 175
Db 286 VIMHTIFQERDLTKFKIPVDLTITLMTLEDHYADVAHNNIHAADVQSTHVLSTP 345
QY 176 KLANSVTPMDILLSLIAAATHDLDPGVNQPFLLKTNHYLATYKNTSVLENHHRSAVG 235
Db 346 ALAEAVTDLEILAAIFASAIHDVDPGVSNQFLINTNSALMYNDSSVLENHHLAVGFK 405
QY 236 LIRESG--LFSHLPLESRQOMETQIGALILATDISRQNEVLSLFRSHLD-----RGDLC 287
Db 406 LLQENCDIFQNLTKKQSLRKAIDIVLATDMSKHMLLADLTKMTVETKVTSSGVLL 465
QY 288 LEDTRHRLVLMALKACADICNCRTWELSKQWSEKVEFFHQGDIEKKYHLGVSPCLD 347
Db 466 LDNYSRIQVLMNVHCADLSNPTKPLQLYROWTDRIMEEFFRQGRERERGMWISPMCD 525
QY 348 RHETSIANIQIGPMTYVPEPLTEWA 373
Db 526 KINASVEKSOVGFIDYIVHPLWETWA 551

RESULT 13

S71626

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific - human
N/Alternate names: 3',5'-cyclic AMP phosphodiesterase

C/Species: Homo sapiens (man)

C/Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 17-Nov-2000

C/Accession: S71626; I61356

R/Engels, P.; Sullivan, M.; Mueller, T.; Luebbert, H.

FEBS Lett. 358, 305-310, 1995

A/Title: Molecular cloning and functional expression in yeast of a human cAMP-specific P

A/Reference number: S71626; MUID:95145731; PMID:7843419

A/Accession: S71626

A/Molecule type: DNA

A/Residues: 1-712 <ENG>

A/Cross-references: EMBL:Z46632; NID:G727222; PIDN:CAA86601.1; PID:G727223

A/Experimental source: substantia nigra

R/Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,

Mol. Cell. Biol. 13, 6558-6571, 1993

A/Title: A family of human phosphodiesterases homologous to the dunce learning and memoi

A/Reference number: A54442; MUID:94019330; PMID:8413254

A/Accession: I61356

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 462-712 <RES>

A/Cross-references: GB:L20968; NID:G347125; PIDN:AAA03591.1; PID:G347126

C/Genetics:

A/Gene: HSPDE4C1

C/Function:

A/Description: cAMP hydrolysis; converts cAMP to non-cyclic AMP

A/Pathway: cyclic nucleotide metabolism

A/Note: expressed in various tissues but not in cells of the immune system

C/Suprafamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'

C/Keywords: phosphoric diester hydrolase

F:387-615/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match

Best Local Similarity 23.9%; Score 536; DB 2; Length 712;

Matches 123; Conservative 70; Mismatches 153; Indels 24; Gaps 7;

QY 22 ESERGGSH--PYIDFRPHSQSEIEV-SVSARNIRLLSFQYLRSSFRFGTAVNSLN 78

DB 250 ETSRSGNQVSEYISRTFLDQCEVELPKVTAEAPQMS-----RISG-LHGLCHSASLS 303

QY 79 I-----LDDYNGQAKCMLEKVGNNWFDIFLDRLTNGNSLVSLTFHLFSLHGLIEYF 131

DB 304 SATVPRFGVQTQDEQLAKELEDTNKGLDVFKVADVSGNRPLTAIFISFOERDLKTF 363

QY 132 HLDMMKLRFRVMIQEDYHSQNPYHNAADVTQAMHCYLPKPKLANSVTPWDILLSLI 191

DB 364 QIPADTLATYLLMLEGHYHNAVYHNSLHAADVAQSTHVLLATPALEAVFTDLEILAALF 423

QY 192 AAATHDLDHPGVNQPLIKTNHYLATLYKNTSVLENHNRSAVGLLRSG--LFSHLPLE 249

DB 424 ASAIHDVDPGVSNQFLINTNSDVALMYNDASVLENHNLAVGFKLLQAEACDFQNLAK 483

QY 250 SROQMETQIGALITADISRQNEYLSLFRSHLDR-----GDLCELTDRHRLVLMALK 303

DB 484 QSLSRMVIDMVLATDSKMSKMLLADLKTMTVETKVTSLGVLLLDNYSGRIVQLNVLH 543

QY 304 CADICNPCTWELSKQWSEKVTPEFFHQGDTEKKYHGVSPCLDRHTESIANIQIGFMTY 363

DB 544 CADLSNFTPLPYRQWTRIMAEFFQGDREGLDISPMCDKHTASVEKSVQGFIDY 603

QY 364 LVEPLFTWA 373

DB 604 IAHPLWETWA 613

RESULT 14

I67945

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) - rat (fragment)

N/Alternate names: cAMP phosphodiesterase 1

C/Species: Rattus norvegicus (Norway rat)

C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Nov-2000

C/Accession: I67945; A33904

R/Bolger, G.B.; Rodgers, L.K.; Riggs, M.

Gene 149, 237-244, 1994

A/Title: Differential CNS expression of alternative mRNA isoforms of the mammalian gene

A/Reference number: I53865; MUID:95047482; PMID:7958996

A/Accession: I67945

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-536 <RES>

A/Cross-references: GB:L27061; NID:G436011; PIDN:AAA56858.1; PID:G436012

R/Swinnen, J.V.; Joseph, D.R.; Conti, M.

Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989

A/Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP

A/Reference number: A33904; MUID:89315790; PMID:2546153

A/Accession: A33904

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 230-496 <SWI>

A/Cross-references: GB:M25347; GB:M28410

C/Suprafamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'

C/Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase

F:253-481/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match

Best Local Similarity 23.2%; Score 534.5; DB 2; Length 536;

Matches 118; Conservative 71; Mismatches 159; Indels 19; Gaps 6;

QY 22 ESERGGSH--PYIDFRPHSQSEIEVSVARN-----IRLLSFQYLRSSFRFGTAVS 74

DB 117 ETSRSGNQVSEYISQTFDQQAELVELPAPPTEDHPWMAQITGLRKSCHTS---LPTAAI 173

QY 75 NSLITLDDYNGQAKCMLEKVGNNWFDIFLDRLTNGNSLVSLTFHLFSLHGLIEYFHL 134

DB 174 PRFGVQTQDEQLAK-ELEDTNKWGLDVFKVLESGNRPLTAVIPLVQLERDLTKTFQ 232

QY 135 MMKLRFRVMIQEDYHSQNPYHNAADVTQAMHCYLPKPKLANSVTPWDILLSIAA 194

DB 233 ADTLRYLLTLRGHYHNAVYHNSLHAADVAQSTHVLLATPALEAVFTDLEILAALFACA 292

QY 195 THDLDPGVNQPLIKTNHYLATLYKNTSVLENHNRSAVGLLR--ESGLFSLHPLSRQ 252

DB 293 IHDVDPGVSNQFLINTNSLSEALMYNDSSVLENHNLAVGFKLLQGENCDFQNLSTKQK 352

QY 253 QMETQIGALITADISRQNEYLSLFRSHLDR-----GDLCELTDRHRLVLMALKCAD 306

DB 353 SLRRMVIDMVLATDSKMSKMLLADLKTMTVETKVTSLGVLLLDNYSGRIVQLVQLVHCAD 412

QY 307 ICNCPCTWELSKQWSEKVTPEFFHQGDTEKKYHGVSPCLDRHTESIANIQIGFMTY 366

DB 413 LSNPAKPLPYRQWTRIMAEFFQGDREGLDISPMCDKHTASVEKSVQGFIDYIAH 472

QY 367 PLFTWA 373

DB 473 PLWETWA 479

RESULT 15

JW0088

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 8A, high affinity cAMP-specific

N/Alternate names: high affinity cAMP-specific phosphodiesterase PDE8A

C/Species: Homo sapiens (man)

C/Date: 18-Jun-1998 #sequence_revision 26-Aug-1999 #text_change 21-Jul-2000

C/Accession: JW0088

R/Fisher, D.A.; Smith, J.F.; Pillar, J.S.; St Denis, S.H.; Cheng, J.B.

Biochem. Biophys. Res. Commun. 246, 570-577, 1998

A/Title: Isolation and characterization of PDE8A, a novel human cAMP-specific phosphod.

A/Reference number: JW0088; MUID:98289571; PMID:9618252

A/Accession: JW0088

A/Molecule type: mRNA

A/Residues: 1-713 <PISA>

A/Cross-references: GB:AF056490; NID:G3184388; PIDN:AA39763.1; PID:G3184389

C/Suprafamily: 3',5'-cyclic-nucleotide phosphodiesterase 8A, high affinity cAMP-specific

C/Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase

F;439-680/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
 Query Match 22.4%; Score 503; DB 2; Length 713;
 Best Local Similarity 31.6%; Pred. No. 2.6e-33;
 Matches 117; Conservative 76; Mismatches 145; Indels 32; Gaps 7;

QY	54	RLLSFORYLRSRRFGRTAVSNSINILID---- <td>109</td>	109
DB	338	RLLSGNEYVLST---KNTQWVSS-NIITPISLDDVPPRIARAMENBEYWFDFIFELEAAT	393
QY	110	NGNSLVSLTTHLPSLGLIIEYFHLDDMMKLRRLVMIQEDYHSONPYHNAVHAADVTQAMH	169
DB	394	HNRPLIYLGKMFARFGICEFLHCSESTLRSWLQIIEANYHSSNPYHNSHSDVILHATA	453
QY	170	CYLKEPKLANSVTPWDILLSLIAAATHDLDPGVNQPPFLIKTNHYLATYKNTSVLENHH	229
DB	454	YFLSKRIKETLPIDIEVAALIAATHDVPHTNSFLCNAGSELAALLYNDTAVLESHH	513
QY	230	WRSAGVGLLR---ESGLFSLPLESRQOMETQIGALILATDISRQNEYLSLFRSHLDRGDL	286
DB	514	AALAFQLTTGDDKCNIFKNMERNDYRTLROGIIDMVLATEMTKFEHVNFVNSINKPLA	573
QY	287	CLEDT-----RHRHLVLOALKACADICNPCRTELKSKWSEKVTDEFF	329
DB	574	TLBENGETDKNQEVINTMLTPTENRTLIKMLIKCADVSNPCRPLOQYCIENAAARISEYF	633
QY	330	HQGDIEKKYHLG-VSPCLDRHTESIANIQIGFMTYLVEPLFTWARFENRSLQTMIGHV	388
DB	634	SQTDEEKQOGLPVVMPVFDNRTCSIPKSIQISFDYFITDMEDAWDAFVDL---PDLMQHL	690
QY	389	GIANKASWKGL 398	
DB	691	DNNFKYWKGL 700	

Search completed: May 26, 2004, 09:25:36
 Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2004, 09:24:28 ; Search time 46 Seconds
(without alignments)
2921.973 Million cell updates/sec

Title: US-09-966-781A-1

Perfect score: 2243

Sequence: 1 DQALYIRMLGQVVRVSRA.....DTDAAFELNSQLLPQENRLS 426

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp archaea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
7: sp mhc:*
8: sp organelle:*
9: sp phage:*
10: sp plant:*
11: sp rodent:*
12: sp virus:*
13: sp vertebrate:*
14: sp unclassified:*
15: sp rvirus:*
16: sp bacteriap:*
17: sp archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1910	85.2	424	4 Q96T72	Q96T72 homo sapien
2	1389.5	61.9	446	11 Q8VIE4	Q8VIE4 rattus norv
3	1377.5	61.4	422	4 Q9BZ40	Q9BZ40 homo sapien
4	1377.5	61.4	446	11 Q8CBS2	Q8CBS2 mus musculus
5	1377.5	61.4	459	11 Q8VIE2	Q8VIE2 rattus norv
6	1231.5	54.9	359	11 Q8VIE3	Q8VIE3 rattus norv
7	717	32.0	162	4 Q86V65	Q86V65 homo sapien
8	555	24.7	771	11 Q9EQR7	Q9EQR7 rattus norv
9	551	24.6	721	11 Q9QXI7	Q9QXI7 mus musculus
10	550	24.5	542	11 Q91VY2	Q91VY2 mus musculus
11	550	24.5	606	4 Q13945	Q13945 homo sapien
12	550	24.5	659	11 Q8VD81	Q8VD81 rattus norv
13	550	24.5	721	11 Q8VBU5	Q8VBU5 mus musculus
14	550	24.5	736	11 Q8VD82	Q8VD82 rattus norv
15	548	24.4	667	4 Q81V84	Q81V84 homo sapien
16	545	24.3	518	4 Q43850	Q43850 homo sapien

17	545	24.3	700	4 P78505	P78505 homo sapien
18	545	24.3	782	4 Q76105	Q76105 homo sapien
19	545	24.3	791	4 Q43849	Q43849 homo sapien
20	543	24.2	584	11 Q8C4Q7	Q8C4Q7 mus musculus
21	543	24.2	747	11 Q8CG05	Q8CG05 mus musculus
22	542	24.2	518	4 Q81VD3	Q81VD3 homo sapien
23	542	24.2	679	4 Q722L8	Q722L8 homo sapien
24	542	24.2	748	4 Q81VD2	Q81VD2 homo sapien
25	541	24.1	647	4 Q81VA7	Q81VA7 homo sapien
26	541	24.1	825	4 Q9H3H2	Q9H3H2 homo sapien
27	539	24.0	517	11 Q8CG06	Q8CG06 rattus norv
28	539	24.0	747	11 Q8CG04	Q8CG04 rattus norv
29	539	24.0	803	11 Q35470	Q35470 rattus norv
30	538	24.0	518	4 Q81VA9	Q81VA9 homo sapien
31	535	23.9	426	4 Q9UPJ5	Q9UPJ5 homo sapien
32	503	22.4	829	4 Q96T71	Q96T71 homo sapien
33	500	22.3	383	11 Q8BQB2	Q8BQB2 mus musculus
34	493.5	22.0	599	5 Q81FZ3	Q81FZ3 caenorhabdi
35	493.5	22.0	612	5 Q86NE9	Q86NE9 caenorhabdi
36	493.5	22.0	626	5 Q95ZQ6	Q95ZQ6 caenorhabdi
37	493.5	22.0	674	5 Q86NE8	Q86NE8 caenorhabdi
38	478	21.3	521	5 Q8MRN3	Q8MRN3 drosophila
39	478	21.3	624	5 Q9W4S8	Q9W4S8 drosophila
40	478	21.3	629	5 Q81RU5	Q81RU5 drosophila
41	478	21.3	642	5 Q81RU6	Q81RU6 drosophila
42	478	21.3	662	5 Q81RU4	Q81RU4 drosophila
43	478	21.3	711	5 Q81RU7	Q81RU7 drosophila
44	478	21.3	776	5 Q81RU8	Q81RU8 drosophila
45	478	21.3	778	5 Q81RU9	Q81RU9 drosophila

ALIGNMENTS

RESULT 1

Q96T72 ID Q96T72 PRELIMINARY; PRT; 424 AA.
AC Q96T72;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE CAMP-specific cyclic nucleotide phosphodiesterase PDE7A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21265457; PubMed=11371644;
RA Glavas N.A., Ostenson C., Schaefer J.B., Vasta V., Beavo J.A.;
RT "T cell activation up-regulates cyclic nucleotide phosphodiesterases 8A1 and 7A3";
RL Proc. Natl. Acad. Sci. U.S.A. 98:6319-6324 (2001).
DR EMBL; AF332652; AAK57640.1; -;
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . . ; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met_phosphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PRO0387; PDIESTERASE1.
DR SMART; SM00471; Hdc; 1.
DR PROSITE; PS00126; PDEASE I; 1.
SQ SEQUENCE 424 AA; 48827 MW; A7DBF40D08A7B561 CRC64;

Query Match 85.2%; Score 1910; DB 4; Length 424;

Best Local Similarity 99.5%; Pred. No. 8.4e-164;

Matches 362; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DQALYIRMLGQVVRVSRAFGESRRGSHYPIDFRIFHSQSEIEVSVSARNIRLLSFOR 60

DB 57 DQALYIRMLGQVVRVSRAFGESRRGSHYPIDFRIFHSQSEIEVSVSARNIRLLSFOR 116

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QY 61 YLRSSRRFRGTAAGNSLNILDDYNGQAKMLEKVGWNNDFIFLFDRLTNGNSLVSTFFH 120
DB 117 YLRSSRRFRGTAAGNSLNILDDYNGQAKMLEKVGWNNDFIFLFDRLTNGNSLVSTFFH 176
QY 121 LFSHLGLIEYFHLDMKRLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYKPEKPLANS 180
DB 177 LFSHLGLIEYFHLDMKRLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYKPEKPLANS 236
QY 181 VTPWDIILSLTAAATHDLDHGVNQPFLIKTNHVLATLYKNTSVLENHHWRSVAGLLRES 240
DB 237 VTPWDIILSLTAAATHDLDHGVNQPFLIKTNHVLATLYKNTSVLENHHWRSVAGLLRES 296
QY 241 GLFSLPLESRQOMETOIGALILATDISRQNEYLSLFRSHLDGRDGLCLEDTRHRLVLOM 300
DB 297 GLFSLPLESRQOMETOIGALILATDISRQNEYLSLFRSHLDGRDGLCLEDTRHRLVLOM 356
QY 301 ALKADICNCPRTWELSKQSEKVTBFFHQGDIEKKYHGVSPCLDRHTESIANIQIGF 360
DB 357 ALKADICNCPRTWELSKQSEKVTBFFHQGDIEKKYHGVSPCLDRHTESIANIQIGF 416
QY 361 MTYL 364
DB 417 YTYL 420
RESULT 2
Q8VIE4
ID Q8VIE4 PRELIMINARY; PRT; 446 AA.
AC Q8VIE4; 2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BA472E5.1 (High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase
GN RNPDE7B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Sasaki T., Kotera J., Omori K.;
RT "Novel alternative splice variants of rat PDE7B."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB057409; BAB79637.1; -
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . . ; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met_pshphohydro.
DR Pfam; PF002073; PDEase.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase.
SQ SEQUENCE 446 AA; 51475 MW; 01567BDABC905D19 CRC64;

Query Match 61.9%; Score 1389.5; DB 11; Length 446;
Best Local Similarity 62.4%; Pred. No. 8.9e-117;
Matches 257; Conservative 65; Mismatches 95; Indels 5; Gaps 2;

QY 1 DQATYTRMLGDVVRSGAPESERRGSHPIYDPRIFHSQSEIEVSVARNIRLLSFQR 60
DB 18 EQNVKVCMLGDVRLRGQTGVPARRGSGYPIDFRLNNTTSHSGEIGSKKKVRLLSFQR 77
QY 61 YLRSSRRFRGTAAGNSLNILDDYNGQAKMLEKVGWNNDFIFLFDRLTNGNSLVSTFFH 120
DB 78 HFHESLLRGMTPOAPLHLLDEDYLGQARHMLSKVGWMDDFIFLFDRLTNGNSLVTLCH 137
QY 121 LFSHLGLIEYFHLDMKRLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYKPEKPLANS 180
DB 138 LFSHGLIHHFKLDMVTLHRLVLMVQEDYHGHNPYHNAVHAADVTQAMHCYKPEKPLAS 197
QY 181 VTPWDIILSLTAAATHDLDHGVNQPFLIKTNHVLATLYKNTSVLENHHWRSVAGLLRES 240

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DB 198 LTPDLIMGLGAAAHDDVHPGVNQPFLIKTNHHLANLYQNMVLENHHRSTRIGMLRES 257
QY 241 GLFSLPLESRQOMETOIGALILATDISRQNEYLSLFRSHLDGRDGLCLEDTRHRLVLOM 300
DB 258 RLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRKALHNLKLENIQDRHFMLOI 317
QY 301 ALKADICNCPRTWELSKQSEKVTBFFHQGDIEKKYHGVSPCLDRHTESIANIQIGF 360
DB 318 ALKADICNCPRTWELSKQSEKVTBFFHQGDIEKKYHGVSPCLDRHTESIANIQIGF 377
QY 361 MTYLVEPLFEWARFS-NTRLSTOTMLGHVGLNKASKWGL---QREGSSSED 407
DB 378 MTYLVEPLFEWARFNGTSLSESMLNHLAHLAKQWKSLLSNQHRRGSGQD 429
RESULT 3
Q9BZ40
ID Q9BZ40 PRELIMINARY; PRT; 422 AA.
AC Q9BZ40; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BA472E5.1 (High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase
GN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cobley V.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL138628; CAC27545.1; -
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . . ; IEA.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met_pshphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF002073; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW NON-TER
SQ SEQUENCE 422 AA; 48718 MW; B5E263725119A64D CRC64;

Query Match 61.4%; Score 1377.5; DB 4; Length 422;
Best Local Similarity 62.8%; Pred. No. 1e-115;
Matches 252; Conservative 65; Mismatches 83; Indels 1; Gaps 1;

QY 12 DVVRSGAPESERRGSHPIYDPRIFHSQSEIEVSVARNIRLLSFQRVLRSPFRGT 71
DB 1 DLRGQTGVPARRGSGYPIDFRLNNTTSGEIGTKKKVRLLSQRYFHASRLRGI 60
QY 72 AVNSNLILDDYNGQAKMLEKVGWNNDFIFLFDRLTNGNSLVSTFFHLSHGLIEYF 131
DB 61 IPOAPLHLLDEDYLGQARHMLSKVGWMDDFIFLFDRLTNGNSLVTLCHFNTHGLIHF 120
QY 132 HLDMMKRLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYKPEKPLANSVTPWDILSLI 191
DB 121 KLDWVTLHRLVLMVQEDYHSQNPYHNAVHAADVTQAMHCYKPEKPLASFLTPDILMGLL 180
QY 192 AAATHLDHGVNQPFLIKTNHVLATLYKNTSVLENHHWRSVAGLLRESGLFHLPLESR 251
DB 181 AAAAHDDVHPGVNQPFLIKTNHHLANLYQNMVLENHHRSTRIGMLRESLHLPKEMT 240
QY 252 QOMETOIGALILATDISRQNEYLSLFRSHLDGRDGLCLEDTRHRLVLOMALKKADICNCP 311
DB 241 QDIEQQJGSLILATDINRQNEFLTRKALHNLKLENIQDRHFMLOIALKKADICNCP 300
QY 312 RTWELSKQSEKVTBFFHQGDIEKKYHGVSPCLDRHTESIANIQIGFMTYLVPELTFE 371

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Db 301 RLWENSKQWSEVCEFFYQGLEQKFELEISPLCNQKQDSIPSIQIGWMSVIVPELFE 360
QY Q8CBS2 PRELIMINARY; PRT; 446 AA.
AC Q8CBS2;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Phosphodiesterase 7B.
GN PDE7B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK035385; BAC29052.1; -.
DR MGD; MGI:1352752; Pde7b.
DR GO; GO:0004115; F-cAMP-specific phosphodiesterase activity; IDA.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 446 AA; 51307 MW; 7C002364B396A5A8 CRC64;

Query Match 61.4%; Score 1377.5; DB 11; Length 446;
Best Local Similarity 61.9%; Pred. No. 1.1e-115;
Matches 255; Conservative 67; Mismatches 85; Indels 5; Gaps 2;

QY 1 DGTALYRMGLDVRSRAGFSESGHPYIDFRIFHSQSEIEVSARNRRLLSFOR 60
Db 18 EOSVXCVCMGLDVRLRGQGVPAERRGSYFFIDFRLNNTTHSGEIGTKKKVRLLSFOR 77
QY 61 YLRSRFRFGTAVSNILDDYNGQAKMLEKVGNNMFDIFLFDRLTNGNSLVSLTFH 120
Db 78 YFHASRLLAGIIPQAPLHLLDDYLGQARHMLSKVGTWDFLFDRLTNGNSLVLLCH 137
QY 121 LFSHGLIYFHLDMKMLRFLVMIOEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
Db 138 LFNSHGLIHFFKLDVMVTLFRFLVMVQEDYHGNPNYHNAVHAADVTQAMHCYLKEPKLAS 197
QY 181 VFPWDILLSLIAAATHDHPGVNQPFLLKTNHLYLATYKNTSVLENHWRSAVGLLRSS 240
Db 198 LFPDLMLGLAAAADVHPGVNQPFLLKTNHLYLATYKNTSVLENHWRSAVGLLRSS 257
QY 241 GLFSLHPLSRQOMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRLHVLQM 300
Db 258 RULLAHLPEKMTQDIEQQLGSLILATINRQNEFLTRKLAHLNKLRLLENVQDRHFMQLI 317
QY 301 ALKCADICNPCTWELSKWSEKVTVEEPHQGDIEKKYHLGVSPCLDRHTESIANIQIGF 360
Db 318 ALKCADICNPCTWELSKWSEKVTVEEPHQGDIEKKYHLGVSPCLDRHTESIANIQIGF 377
QY 361 MYVLEPFLTEWAFRS-NTRLSQTMGLGHVGLNKAWSKGL- ---QRESSSED 407
Db 378 MYVLEPFLTEWAFRS-NTRLSQTMGLGHVGLNKAWSKGL- ---QRESSSED 429

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RESULT 5
Q8VIE2 PRELIMINARY; PRT; 459 AA.
AC Q8VIE2;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Cyclic nucleotide phosphodiesterase 7B4 (EC 3.1.4.17).
GN RNPDE7B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Sasaki T., Kotera J., Omori K.;
RT "Novel alternative splice variants of rat PDE7B."
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB057411; BAB79639.1; -.
DR GO; GO:0004114; F3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0016787; F-hydrolase activity; IEA.
DR GO; GO:0007165; P-signal transduction; IEA.
DR InterPro; IPR003607; Met phosphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase.
SQ SEQUENCE 459 AA; 52680 MW; A3F26E95C7FC00A5 CRC64;

Query Match 61.4%; Score 1377.5; DB 11; Length 459;
Best Local Similarity 63.2%; Pred. No. 1.1e-115;
Matches 254; Conservative 63; Mismatches 80; Indels 5; Gaps 2;

QY 11 GQVRSRAGFSESGHPYIDFRIFHSQSEIEVSARNRRLLSFORILSSRFFRG 70
Db 41 GQVRLRGQGVPAERRGSYFFIDFRLNNTTHSGEIGSKKKVRLLSFORHSHESLLRG 100
QY 71 TAVSNILDDYNGQAKMLEKVGNNMFDIFLFDRLTNGNSLVSLTFHLSHGLIY 130
Db 101 MTPQAPLHLLDDYLGQARHMLSKVGTWDFLFDRLTNGNSLVLLCHLFSHGLIHH 160
QY 131 FHLDMKMLRFLVMIOEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSL 190
Db 161 FKLDVMVTLFRFLVMVQEDYHGNPNYHNAVHAADVTQAMHCYLKEPKLASFLPLDMLGL 220
QY 191 IAAATHDHPGVNQPFLLKTNHLYLATYKNTSVLENHWRSAVGLLRSSGLFSHPLRS 250
Db 221 LAAAHADVHPGVNQPFLLKTNHLYLATYKNTSVLENHWRSTIGWLRSSRLAHLPEK 280
QY 251 RQOMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRLHVLQMAKCADICNP 310
Db 281 TQDIEQQLGSLILATINRQNEFLTRKLAHLNKLRLLENVQDRHFMQLIQLKCADICNP 340
QY 311 CRTWELSKWSEKVTVEEPHQGDIEKKYHLGVSPCLDRHTESIANIQIGFMYVLEPFL 370
Db 341 CRTWELSKWSEKVTVEEPHQGDIEKKYHLGVSPCLDRHTESIANIQIGFMYVLEPFL 400
QY 371 EWAFRS-NTRLSQTMGLGHVGLNKAWSKGL- ---QRESSSED 407
Db 401 EWARTGNSTLSSEMLNHLAHLNKAQWKSLLSNQHRRRSGSQD 442

RESULT 6
Q8VIE3 PRELIMINARY; PRT; 359 AA.
AC Q8VIE3;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)

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RL Invest. Ophthalmol. Vis. Sci. 40:1745-1752(1999).
[2]
RN
RP SEQUENCE FROM N.A.
RA Zhou L., Thompson W.J., Potter D.E.;
RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY266364; AAP31236.1; -.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR DR InterPro; IPR002073; PDEase.
DR NON_TER 1
FT NON_TER 162 162
SQ SEQUENCE 162 AA; 18867 MW; E7D548571291EEDA CRC64;
Query Match 32.0%; Score 717; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.1e-56;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DOTALYRMLGDVVRVSRAGFESRRGSHPYIDFRIFHSQSEIEVSVARNIRLLSFQR 60
DB 24 DOTALYRMLGDVVRVSRAGFESRRGSHPYIDFRIFHSQSEIEVSVARNIRLLSFQR 83
QY 61 YLRSSFFRGTAVNSNLILDDYNGQAKMCKVGNWNPDIPLFRLTNGNSLVSLTFH 120
DB 84 YLRSSFFRGTAVNSNLILDDYNGQAKMCKVGNWNPDIPLFRLTNGNSLVSLTFH 143
QY 121 LFSLHGLIEYFHLDMMKLR 139
DB 144 LFSLHGLIEYFHLDMMKLR 162
RESULT 8
Q9EQR7 PRELIMINARY; PRT; 771 AA.
AC Q9EQR7
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Cyclic AMP phosphodiesterase PDB4A10 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RA Rena G., Begg F., Ross A., MacKenzie C., McPhee I., Campbell L.,
RA Huston E., Sullivan M., Houslay M.D.;
RL "Molecular cloning, genomic positioning, promoter identification and
RL characterisation of the novel cAMP-specific phosphodiesterase,
RL PDB4A10.";
RL Mol. Pharmacol. 0:0-0(2001).
DR EMBL; AF114461; AAF14352.2; -.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003894; P:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met_Phsphohydro.
DR DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
FT NON_TER 1
FT NON_TER 771 771
SQ SEQUENCE 771 AA; 85459 MW; D20712E515CDAF0B CRC64;
Query Match 24.7%; Score 555; DB 11; Length 771;
Best Local Similarity 32.6%; Pred. No. 4.2e-41;
Matches 127; Conservative 77; Mismatches 154; Indels 32; Gaps 7;
QY 8 RMLGDVVRVSRAGFESRRGSHPYIDFRIFHSQSEIEVSVARNIRLLSFQR----YLR 63
DB 190 RELTSLSEMSRSGNQSVYIINTFLD-----KONEVEIPSPTRQR---AFQPPPSVLR 241
QY 64 SSP-----FRFGTAVNSNIN-----LDDYNGQAKMCKVGNWNPDIPLFRLTNG 111

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Db 242 OSQPMQSTGLKULVHTGSLNTNTPRFVKTQDQEDLLAQELENISKWGLNIFCVSEYAGG 301
 QY 112 NSLSVLTFLHSLHGLIEYFHLDMKMLRFLVMIQEDYHSQNPYHNAVHAADVTQAMECY 171
 Db 302 RSLSCIMYTIQERDLAKKEHLPVDTMMYMLTLBHDYHADVAYHNSLHAADVLSQSTHVL 361
 QY 172 LKEPKLANSVTPWDILLSIAAATHDHPGVNQFLLKTNHYLATLYKNTSVLENHHR 231
 Db 362 LATPALDAVFTDLETLAALFAAITHDHPGVSNQFLINTNSLALMYNDESVLNHHLA 421
 QY 232 SAVGLRESG--LFSHLPESRQOMETOIGALILATDISRQNEYLISLFRSHLD-----R 283
 Db 422 VGFKLQENCDIFQNLKSRQORSLRKVVIDMVLATDMSKMTLLADLKTNVETKVTSS 481
 QY 284 GDLCLDTRHRLVLMALKKADI CNPCKTWELSKQWSEKVTTEFFHQGDIEKKVHLGVS 343
 Db 482 GVLLLDNYSRDIQVLRNMVHCADLSNPTKSLRYQWTDRIAEFFQOQDRERGRGMEIS 541
 QY 344 PLCDRHTEISIANIQGFMTYLVPLFTWA 373
 Db 542 PMCDKHTASVEKSVQGFIDYIVHPLMETWA 571

RESULT 9

Q9QXI7 PRELIMINARY; PRT; 721 AA.
 ID AC Q9QXI7
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CAMP-specific phosphodiesterase (Phosphodiesterase 4B, CAMP specific).
 DE PDE4B.
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SWISS WEBSTER;
 RA Cherry J.A., Thompson B.E., Pho V.;
 RT "Cloning and biochemical characterization of cyclic AMP phosphodiesterase isoforms in the mouse."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SWISS WEBSTER;
 RA Cherry J.A., Thompson B.E., Pho V.;
 RT "Diazepam and rolipram differentially inhibit CAMP-specific phosphodiesterases PDE4A1 and PDE4B3 in the mouse."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF208023; AAF19202.2; -
 DR EMBL; AJ297397; CAB96770.1; -
 DR MGD; MGI:99557; Pde4b.
 DR GO; GO:0004114; F:3'; 5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR003607; Met phosphohydro.
 DR Pfam; PF00233; PDEase; 1.
 DR PRINTS; PR00387; PDIESTERASE1.
 DR SMART; SM00471; Hdc; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 SQ SEQUENCE 721 AA; 82074 MW; 302311CA44636E7F CRC64;

Query Match 24.6%; Score 551; DB 11; Length 721;
 Best Local Similarity 31.8%; Pred. No. 8.7e-41;
 Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;
 QY 8 RMLGDVVRVRAGFESERRGSHYIDRIFHSQSEIEVSVSARNIR-----LLSF 58
 Db 241 RELTHLSEMSRSGNVSEYISNTFLD-----KQNDVEIPSPQDKREKKKQQLMTQISG 295

QY 59 QRYLRSRFRFGTAVSN-SLNILDDDYNGQAKCMLEKVGNNWFDIFLDRLTNGNSIVSL 117
 Db 296 VKLKHSSLNNTSIRFGINTENEDHLAKE---LEDLNKGLNLFNVAGYSHNRPLCI 352
 QY 118 TFHLFSLHGLIEYFHLDMKMLRFLVMIQEDYHSQNPYHNAVHAADVTQAMECYLKEPKL 177
 Db 353 MYAIFQERDLAKKEHLPVDTMMYMLTLBHDYHADVAYHNSLHAADVLSQSTHVLSTPAL 412
 QY 178 ANSVTPWDILLSIAAATHDHPGVNQFLLKTNHYLATLYKNTSVLENHHRSAVGLL 237
 Db 413 DAVFTDLETLAALFAAITHDHPGVSNQFLINTNSLALMYNDESVLNHHLA VGFKL 472
 QY 238 RES--GFSLHPLESRQOMETOIGALILATDISRQNEYLISLFRSHLD-----RGDLCL 289
 Db 473 QEEHCDIFQNLKSRQORSLRKVVIDMVLATDMSKMTLLADLKTNVETKVTSSGVLLLD 532
 QY 290 DTRHRLVLMALKKADI CNPCKTWELSKQWSEKVTTEFFHQGDIEKKVHLGVSPLCDRH 349
 Db 533 NYTDRIQVLRNMVHCADLSNPTKSLRYQWTDRIAEFFQOQDRERGRGMEISPMCDKH 592
 QY 350 TESIANIQGFMTYLVPLFTWA 373
 Db 593 TASVEKSVQGFIDYIVHPLMETWA 616

RESULT 10

Q91VY2 PRELIMINARY; PRT; 542 AA.
 ID Q91VY2
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to phosphodiesterase 4B, cAMP-specific (Dunce (Drosophila)-homolog phosphodiesterase E4) (Fragment).
 DE PDE4B OR EDNRA.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast tumor;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC007155; AAH07155.1; -
 DR MGD; MGI:105923; Ednra.
 DR MGD; MGI:99557; Pde4b.
 DR GO; GO:0004114; F:3'; 5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR003607; Met phosphohydro.
 DR InterPro; IPR002073; PDEase.
 DR Pfam; PF00233; PDEase; 1.
 DR PRINTS; PR00387; PDIESTERASE1.
 DR SMART; SM00471; Hdc; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 FT NON TER 1
 SQ SEQUENCE 542 AA; 62279 MW; 8B6296D416275B34 CRC64;

Query Match 24.5%; Score 550; DB 11; Length 542;
 Best Local Similarity 31.8%; Pred. No. 7.2e-41;
 Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

QY 8 RMLGDVVRVRAGFESERRGSHYIDRIFHSQSEIEVSVSARNIR-----LLSF 58
 Db 62 RELTHLSEMSRSGNVSEYISNTFLD-----KQNDVEIPSPQDKREKKKQQLMTQISG 116
 QY 59 QRYLRSRFRFGTAVSN-SLNILDDDYNGQAKCMLEKVGNNWFDIFLDRLTNGNSIVSL 117
 Db 117 VKLKHSSLNNTSIRFGINTENEDHLAKE---LEDLNKGLNLFNVAGYSHNRPLTCI 173
 QY 118 TFHLFSLHGLIEYFHLDMKMLRFLVMIQEDYHSQNPYHNAVHAADVTQAMECYLKEPKL 177

```

Db 174 MYAIFQERDLKTKFKISSDTFFVTMMTELDHYHSDVAYHNSLHAADVAQSTHVLSTPAL 233
QY 178 ANSVTPWDLILLSIAAATHDLHPGVNQPLIKTNHYLATLYKNTSVLENHHSR SAVGLL 237
Db 234 DAVFTDLEILAIAFAAAIHVDHPGVSNQFLINTNSLALMYNDESLENHHLAVGFKLL 293
QY 238 RES--GLFSLHPLSRQOMETOIGALILATDISRQNEYLSLFRSHLD-----RGDLCL 289
Db 294 QEHCDIFQNLTKKQRTLRKMWIDVMTADMSKMSLLADLKTMTVETKVTSSGVLLLD 353
QY 290 DTRHRLVLMALKKADICNPCTRWELSKQWSEKVTFFHQDIEKKYHLGVSPICDRH 349
Db 354 NYTDRIQVLNVMVHCADLSNPTKSLRYQWTDRIEMEEFFQOQDKERERGMELSPMCDKH 413
QY 350 TESIANIQIGFMYLYVEPLFEWA 373
Db 414 TASVEKSQVGFIDYIVHPLMETWA 437

RESULT 11
ID Q13945 PRELIMINARY; PRT; 606 AA.
AC Q13945;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 3',5'-cyclic AMP phosphodiesterase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93314968; PubMed=8392015;
RA Oberholte R., Bhakta S., Alvarez R., Bach C., Mulkins M., Jarnagin K.,
RA Shelton E.R.;
RT "The cDNA of a human lymphocyte cyclic-AMP phosphodiesterase (PDE IV)
RT reveals a multigene family.";
RL Gene 129:239-247(1993).
DR EMBL; L12686; AAA35643.1; -.
DR PIR; JCI519.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met phosphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
DR CAMP.
KW CAMP.
FT NON TER
SQ SEQUENCE 606 AA; 68663 MW; 256BD63B2C79398 CRC64;

Query Match 24.5%; Score 550; DB 4; Length 606;
Best Local Similarity 31.8%; Pred. No. 8.5e-41;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

QY 8 RMLGDVVRVRAGPESRRGSHPYIDPRIFHSQSEIEVSVSARNIR-----LLSF 58
Db 126 RELTHLSMSRSGNQVSEIYISNTFLD-----KQNDVEIPSPQDKREKKKQQLMTQISG 180
QY 59 QRYLRSSRFRGTAVSN--SLNILLDDYNGQAKMELKGVNWNFDIFLDRLTNGNSLVSL 117
Db 181 VKLHMSSSLNNTSISRFVGNVTENEDHLAKE---LEDLKNGLNLFVAGYSHNRPLTCI 237
QY 118 TFHLSLHGLIEFYHLDMMKRLFLVMIQEDYHSQNPYHNAVHAADVTQAMCHYLKEPKL 177
Db 238 MYAIFQERDLKTKFKISSDTFFVTMMTELDHYHSDVAYHNSLHAADVAQSTHVLSTPAL 297
QY 178 ANSVTPWDLILLSIAAATHDLHPGVNQPLIKTNHYLATLYKNTSVLENHHSR SAVGLL 237

Query Match 24.5%; Score 550; DB 11; Length 659;
Best Local Similarity 31.8%; Pred. No. 9.5e-41;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

QY 8 RMLGDVVRVRAGPESRRGSHPYIDPRIFHSQSEIEVSVSARNIR-----LLSF 58
Db 179 RELTHLSMSRSGNQVSEIYISNTFLD-----KQNDVEIPSPQDKREKKKQQLMTQISG 233
QY 59 QRYLRSSRFRGTAVSN--SLNILLDDYNGQAKMELKGVNWNFDIFLDRLTNGNSLVSL 117
Db 234 VKLHMSSSLNNTSISRFVGNVTENEDHLAKE---LEDLKNGLNLFVAGYSHNRPLTCI 290
QY 118 TFHLSLHGLIEFYHLDMMKRLFLVMIQEDYHSQNPYHNAVHAADVTQAMCHYLKEPKL 177
Db 291 MYAIFQERDLKTKFKISSDTFFVTMMTELDHYHSDVAYHNSLHAADVAQSTHVLSTPAL 350
QY 178 ANSVTPWDLILLSIAAATHDLHPGVNQPLIKTNHYLATLYKNTSVLENHHSR SAVGLL 237
Db 351 DAVFTDLEILAIAFAAAIHVDHPGVSNQFLINTNSLALMYNDESLENHHLAVGFKLL 410
QY 238 RES--GLFSLHPLSRQOMETOIGALILATDISRQNEYLSLFRSHLD-----RGDLCL 289
Db 411 QEHCDIFQNLTKKQRTLRKMWIDVMTADMSKMSLLADLKTMTVETKVTSSGVLLLD 470
QY 290 DTRHRLVLMALKKADICNPCTRWELSKQWSEKVTFFHQDIEKKYHLGVSPICDRH 349

```

Db 471 NYTDRIQVLRNMVHCADLSNPTKSLRYQWTDRIWESFFQGGDKXERGMESIPMCDKH 530

QY 350 TESIANIQIGFMTYLVPELFTWA 373
 ID Q8VBU5 PRELIMINARY; PRT; 721 AA.

Db 531 TASVEKSVQGFIDYIVHPLWETWA 554

RESULT 13

Q8VBU5
 ID Q8VBU5 PRELIMINARY; PRT; 721 AA.

AC Q8VBU5;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Phosphodiesterase 4B.
 GN PDE4B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DBA/2J, and C57BL/6J; TISSUE=Brain;
 RA Fehr C., Belknap J.K., Crabbe J.C., Buck K.J.;
 RT "High resolution mapping of a quantitative trait locus for acute
 ethanol withdrawal on mouse chromosome 4 and characterization of
 potential candidate genes";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF326556; AAL37402.1; -;
 DR EMBL; AF326555; AAL37401.1; -;
 DR MGD; MGI:99557; Pde4b
 DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . . ; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR003607; Met phosphohydro.
 DR Pfam; PF00233; PDEase; 1
 DR PRINTS; PRO0387; PDIESTERASE1.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 SQ SEQUENCE 721 AA; 82075 MW; B3725AA78A7612FB CRC64;

Query Match 24.5%; Score 550; DB 11; Length 721;
 Best Local Similarity 31.8%; Pred. No. 1.1e-40;
 Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

QY 8 RMLGVRVRSRAGFESERRGSHPYIDRIFHQSSEIEVSVARNRR-----LLSF 58
 Db 241 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSTQKREKKKQQLMTQISG 295

QY 59 QRYLRSRFRGTAVERN-SLNILDDDDYNGQAKCMLEKVGNNWDFIFDLRLTNGNSLVSL 117
 Db 296 VKKLMHSSSLNNTSISRFVNTENEDHLAKE---LEDLNKWLGNIFNVAGYSHNRPLTCTI 352

QY 118 TFHLSLHGLIEVFLHDMKRLRFLVMIQEDYHSQNPYHNAVAADVTQAMHCYKPEKL 177
 Db 353 MYAIFQERDLTKTKISSDTFTVYMTLEDHYSDVAYHNSLHAADVAQSTHVLSTPAL 412

QY 178 ANSVTPWDILLSIAAATHDLDPGVNQPLIKTNHYLATLYKNTSVLENHNRSAVGLL 237
 Db 413 DAVPTDLEILAAIPAAIHVDHDPGVSNQFLINTNSLALMYNDESLENHLLAVGPKLL 472

QY 238 RES--GLFSLPLESRQOMETQIGALITADISRONYEYLSLFRSHLD-----RGDLCLE 289
 Db 473 QEEHCDFQNLTKKQRTLRKQVDMVLATDMSKHMSLLADLTKMTVETKKVTSSGVLLLD 532

QY 290 DTRHRLVLQALKACADICNPCTRWELSKQSEKVTETEEFHQGDIEKKYHLGVSPCLDRH 349
 Db 533 NYTDRIQVLRNMVHCADLSNPTKSLRYQWTDRIWESFFQGGDKXERGMESIPMCDKH 592

QY 350 TESIANIQIGFMTYLVPELFTWA 373
 Db 593 TASVEKSVQGFIDYIVHPLWETWA 616

RESULT 14

Q8VD82
 ID Q8VD82 PRELIMINARY; PRT; 736 AA.

AC Q8VD82;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE cAMP-specific phosphodiesterase isoform PDE4B1.
 GN PDE4B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
 RA Olsen A.E., Bolger G.B.;
 RT "Novel PDE4B cAMP-specific phosphodiesterase isoforms and related
 technology";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF202732; AAL31763.1; -;
 DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . . ; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR003607; Met phosphohydro.
 DR InterPro; IPR002073; PDEase.
 DR Pfam; PF00233; PDEase; 1.
 DR PRINTS; PRO0387; PDIESTERASE1.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 SQ SEQUENCE 736 AA; 83348 MW; E7850926A8DF169 CRC64;

Query Match 24.5%; Score 550; DB 11; Length 736;
 Best Local Similarity 31.8%; Pred. No. 1.1e-40;
 Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

QY 8 RMLGVRVRSRAGFESERRGSHPYIDRIFHQSSEIEVSVARNRR-----LLSF 58
 Db 256 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSTQKREKKKQQLMTQISG 310

QY 59 QRYLRSRFRGTAVERN-SLNILDDDDYNGQAKCMLEKVGNNWDFIFDLRLTNGNSLVSL 117
 Db 311 VKKLMHSSSLNNTSISRFVNTENEDHLAKE---LEDLNKWLGNIFNVAGYSHNRPLTCTI 367

QY 118 TFHLSLHGLIEVFLHDMKRLRFLVMIQEDYHSQNPYHNAVAADVTQAMHCYKPEKL 177
 Db 368 MYAIFQERDLTKTKISSDTFTVYMTLEDHYSDVAYHNSLHAADVAQSTHVLSTPAL 427

QY 178 ANSVTPWDILLSIAAATHDLDPGVNQPLIKTNHYLATLYKNTSVLENHNRSAVGLL 237
 Db 428 DAVPTDLEILAAIPAAIHVDHDPGVSNQFLINTNSLALMYNDESLENHLLAVGPKLL 487

QY 238 RES--GLFSLPLESRQOMETQIGALITADISRONYEYLSLFRSHLD-----RGDLCLE 289
 Db 488 QEEHCDFQNLTKKQRTLRKQVDMVLATDMSKHMSLLADLTKMTVETKKVTSSGVLLLD 547

QY 290 DTRHRLVLQALKACADICNPCTRWELSKQSEKVTETEEFHQGDIEKKYHLGVSPCLDRH 349
 Db 548 NYTDRIQVLRNMVHCADLSNPTKSLRYQWTDRIWESFFQGGDKXERGMESIPMCDKH 607

QY 350 TESIANIQIGFMTYLVPELFTWA 373
 Db 608 TASVEKSVQGFIDYIVHPLWETWA 631

RESULT 15

Q8IV84
 ID Q8IV84 PRELIMINARY; PRT; 687 AA.

AC Q8IV84;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)

Search completed: May 26, 2004, 09:26:36
Job time : 48 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2004, 09:24:28 ; Search time 97 Seconds
(without alignment)
1240.879 Million cell updates/sec

Title: US-09-966-781a-1
Perfect score: 2243
Sequence: 1 DQALYRMLGDRVRSRAG.....DTDAAFELNSQLLPQENELLS 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2243	100.0	426	5	Aae24527 Human PDE
2	2243	100.0	446	5	Aae24532 Human PDE
3	2243	100.0	482	5	Aae24531 Human PDE
4	2243	100.0	498	2	Aaw00094 CAMP phos
5	2243	100.0	498	2	Aay49808 Human g11
6	2243	100.0	498	3	Aab20619 pTM22 hum
7	2116	94.3	426	5	Aae24529 Rat PDE7
8	2116	94.3	426	5	Aae24533 Rat PDE7a
9	2105	93.8	426	5	Aae24528 Mouse PDE
10	2105	93.8	426	5	Aae24530 Mouse PDE
11	1910	85.2	424	5	Aau79727 Human cyc
12	1903	84.8	432	4	Aau16967 Human nov
13	1787	79.7	336	5	Abb07912 Human PDE
14	1717	76.5	424	5	Aau79713 Human pho
15	1403.5	62.6	450	3	Aay93569 Amino aci
16	1403.5	62.6	450	4	Aau08675 Human pho
17	1403.5	62.6	450	4	Aag78915 Human typ
18	1391.5	62.0	446	3	Aay93567 Amino aci
19	1383.5	61.7	502	5	Abb09005 Human pho
20	1372.5	61.2	502	4	Aab36503 Human lon
21	1360.5	60.7	445	3	Aay93573 Amino aci
22	1358.5	60.6	446	3	Aay93574 Amino aci
23	1358	60.5	451	3	Aay93575 Amino aci
24	1338.5	59.7	437	3	Aay93572 Amino aci
25	1270.5	56.6	413	3	Aay93571 Amino aci

26	1221	54.4	391	4	AAU08676 Human pho
27	1079	48.1	211	4	AAU18681 Renal and
28	1079	48.1	211	4	AAU23004 Novel hum
29	1079	48.1	211	4	AAU17039 Human nov
30	1079	48.1	211	6	ABU97296 Human pol
31	891	39.7	268	3	Aay93593 Amino aci
32	891	39.7	288	3	Aay93568 Amino aci
33	871	38.8	320	4	AAAB36504 Human sho
34	555	24.7	610	2	AAy27197 Rat PDE4A
35	551	24.6	721	6	ABP98434 Amino aci
36	550	24.5	562	2	AAR14836 "Dunce"-1
37	550	24.5	562	2	Aaw00090 Rat dunce
38	550	24.5	562	2	AAy49803 Rat dunce
39	550	24.5	562	3	AAAB20614 Plasmid p
40	550	24.5	564	2	AAR60605 Brain low
41	550	24.5	564	2	AAy49825 Human dun
42	550	24.5	564	3	ABD20636 PDPE32 hu
43	550	24.5	564	3	AAy93994 Amino aci
44	550	24.5	564	4	AAE04745 Rat CAMP-
45	550	24.5	564	6	ABP96788 Human COP

ALIGNMENTS

RESULT 1
AAE24527
ID AAE24527 standard; protein; 426 AA.

XX AAE24527;
XX
XX 04-OCT-2002 (first entry)
XX
XX Human PDE7 protein.
XX
XX Phosphodiesterase 7; PDE7; AIDS; acquired immune deficiency syndrome;
KW immune system disease; enzyme; chronic obstructive pulmonary disease;
KW T-cell related disease; autoimmune disorder; Crohn's disease; cancer;
KW rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
KW colitis; COPD; asthma; therapy; human.
XX
XX Homo sapiens.
XX
XX WO200226954-A2.
XX
XX 04-APR-2002.
XX
XX 28-SEP-2001; 2001WO-EP011303.
XX
XX 28-SEP-2000; 2000EP-00402683.
XX (WARN) WARNER LAMBERT CO.
XX
XX Soulard P;
XX
XX WPI; 2002-479561/51.
XX N-PSDB; AAD39376.
XX
XX Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity
XX than endogenous full length PDE7, for screening of PDE7 inhibitors useful
XX in preventing and treating autoimmune disorders and inflammatory
XX diseases.
XX
XX Claim 2; Page 124-125; 137pp; English.
XX
XX The invention relates to novel polypeptides exhibiting a higher
XX phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length
XX PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of
XX the invention are used for screening compounds that inhibit PDE7
XX activity. PDE7 inhibitors are used for manufacturing a pharmaceutical
XX composition useful for the treatment or prevention of various
XX pathological conditions such as diseases affecting the immune system,
XX including acquired immune deficiency syndrome (AIDS), rejection of

CC transplant, autoimmune disorders such as T-cells related diseases for
CC e.g. rheumatoid arthritis, inflammatory diseases such as respiratory
CC inflammation diseases including chronic obstructive pulmonary disease
CC (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's
CC disease, colitis, pancreatitis and different types of cancers including
CC leukaemia. The present sequence is human PDE7 protein
XX
SQ Sequence 426 AA;

Query Match 100.0%; Score 2243; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 6.3e-226;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQALYIRMLGDVVRVRAGFESERRGSHPIYDIFRIFHSQSEIEVSVSARNIRLLSFQR 60
DB 1 DQALYIRMLGDVVRVRAGFESERRGSHPIYDIFRIFHSQSEIEVSVSARNIRLLSFQR 60

QY 61 YLRSSRFRFGTAVSNSLNILDDYNGQAKCMLEKVGNNFDFLFDRLTNGNSLVSLTFH 120
DB 61 YLRSSRFRFGTAVSNSLNILDDYNGQAKCMLEKVGNNFDFLFDRLTNGNSLVSLTFH 120

QY 121 LFSHLGLIEYFHLDMKLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
DB 121 LFSHLGLIEYFHLDMKLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180

QY 181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWSAVGLLRES 240
DB 181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWSAVGLLRES 240

QY 241 GLFSHLPLESQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTFRHRLVLQM 300
DB 241 GLFSHLPLESQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTFRHRLVLQM 300

QY 301 ALKCADICNPCTWELSKQWSEKVTPEFFHOGDIEKKYHLGVSPICDRHTESIANIQIGF 360
DB 301 ALKCADICNPCTWELSKQWSEKVTPEFFHOGDIEKKYHLGVSPICDRHTESIANIQIGF 360

QY 361 MTYLVEPLFTWARFNSNRLSQTMLGHVGLNKASKWGLQREQSSSEDTDAAAFELNSQLLP 420
DB 361 MTYLVEPLFTWARFNSNRLSQTMLGHVGLNKASKWGLQREQSSSEDTDAAAFELNSQLLP 420

QY 421 QENRLS 426
DB 421 QENRLS 426

RESULT 2
AAE24532
ID AAE24532 standard; protein; 446 AA.
AC AAE24532;
XX
DT 04-OCT-2002 (first entry)

Human PDE7A2 protein.

KW Phosphodiesterase 7; PDE7A2; AIDS; acquired immune deficiency syndrome;
KW immune system disease; enzyme; chronic obstructive pulmonary disease;
KW T-cell related disease; autoimmune disorder; Crohn's disease; cancer;
KW rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
KW colitis; COPD; asthma; therapy; human.
XX
OS Homo sapiens.
XX
XX WO200226954-A2.
XX
XX 04-APR-2002.
XX
XX 28-SEP-2001; 2001WO-EF011303.
XX
XX 28-SEP-2000; 2000EP-00402683.
XX
XX (WARN) WARNER LAMBERT CO.
XX
XX

XX Soulard P;
PI
XX
XX WPI; 2002-479561/51.
XX
PT Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity
PT than endogenous full length PDE7, for screening of PDE7 inhibitors useful
PT in preventing and treating autoimmune disorders and inflammatory
PT diseases.
XX
XX Disclosure; Fig 1; 137pp; English.
PS
XX
XX The invention relates to novel polypeptides exhibiting a higher
CC phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length
CC PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of
CC the invention are used for screening compounds that inhibit PDE7
CC activity. PDE7 inhibitors are used for manufacturing a pharmaceutical
CC composition useful for the treatment or prevention of various
CC pathological conditions such as diseases affecting the immune system,
CC including acquired immune deficiency syndrome (AIDS), rejection of
CC transplant, autoimmune disorders such as T-cells related diseases for
CC e.g. rheumatoid arthritis, inflammatory diseases such as respiratory
CC inflammation diseases including chronic obstructive pulmonary disease
CC (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's
CC disease, colitis, pancreatitis and different types of cancers including
CC leukaemia. The present sequence is human PDE7A2 protein
XX
SQ Sequence 446 AA;

Query Match 100.0%; Score 2243; DB 5; Length 446;
Best Local Similarity 100.0%; Pred. No. 6.8e-226;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQALYIRMLGDVVRVRAGFESERRGSHPIYDIFRIFHSQSEIEVSVSARNIRLLSFQR 60
DB 21 DQALYIRMLGDVVRVRAGFESERRGSHPIYDIFRIFHSQSEIEVSVSARNIRLLSFQR 80

QY 61 YLRSSRFRFGTAVSNSLNILDDYNGQAKCMLEKVGNNFDFLFDRLTNGNSLVSLTFH 120
DB 81 YLRSSRFRFGTAVSNSLNILDDYNGQAKCMLEKVGNNFDFLFDRLTNGNSLVSLTFH 140

QY 121 LFSHLGLIEYFHLDMKLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
DB 141 LFSHLGLIEYFHLDMKLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 200

QY 181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWSAVGLLRES 240
DB 201 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWSAVGLLRES 260

QY 241 GLFSHLPLESQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTFRHRLVLQM 300
DB 261 GLFSHLPLESQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTFRHRLVLQM 320

QY 301 ALKCADICNPCTWELSKQWSEKVTPEFFHOGDIEKKYHLGVSPICDRHTESIANIQIGF 360
DB 321 ALKCADICNPCTWELSKQWSEKVTPEFFHOGDIEKKYHLGVSPICDRHTESIANIQIGF 380

QY 361 MTYLVEPLFTWARFNSNRLSQTMLGHVGLNKASKWGLQREQSSSEDTDAAAFELNSQLLP 420
DB 381 MTYLVEPLFTWARFNSNRLSQTMLGHVGLNKASKWGLQREQSSSEDTDAAAFELNSQLLP 440

QY 421 QENRLS 426
DB 441 QENRLS 446

RESULT 3
AAE24531
ID AAE24531 standard; protein; 482 AA.
XX
AC AAE24531;
XX
DT 04-OCT-2002 (first entry)

XX DE Human PDE7A1 protein.
 XX KW Phosphodiesterase 7; PDE7A1; AIDS; acquired immune deficiency syndrome;
 KW immune system disease; enzyme; chronic obstructive pulmonary disease;
 KW T-cell related disease; autoimmune disorder; Crohn's disease; cancer;
 KW rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
 KW colitis; COPD; asthma; therapy; human.
 XX OS Homo sapiens.
 XX EN WC200226954-A2.
 XX PD 04-APR-2002.
 XX PF 28-SEP-2001; 2001WO-EF011303.
 XX PR 28-SEP-2000; 2000EP-00402683.
 XX (WARN) WARNER LAMBERT CO.
 PA Soulard P;
 XX WPI; 2002-479561/51.
 XX Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity
 PT than endogenous full length PDE7, for screening of PDE7 inhibitors useful
 PT in preventing and treating autoimmune disorders and inflammatory
 PT diseases.
 XX Disclosure; Fig 1; 137pp; English.
 XX The invention relates to novel polypeptides exhibiting a higher
 CC phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length
 CC PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of
 CC the invention are used for screening compounds that inhibit PDE7
 CC activity. PDE7 inhibitors are used for manufacturing a pharmaceutical
 CC composition useful for the treatment or prevention of various
 CC pathological conditions such as diseases affecting the immune system,
 CC including acquired immune deficiency syndrome (AIDS), rejection of
 CC transplant, autoimmune disorders such as T-cells related diseases for
 CC e.g. rheumatoid arthritis, inflammatory diseases such as respiratory
 CC inflammation diseases including chronic obstructive pulmonary disease
 CC (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's
 CC disease, colitis, pancreatitis and different types of cancers including
 CC leukaemia. The present sequence is human PDE7A1 protein
 XX Sequence 482 AA;
 Query Match 100.0%; Score 2243; DB 5; Length 482;
 Best Local Similarity 100.0%; Pred. No. 7.7e-226;
 Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DOTATYIRMLGTVRVRAGFESERRGSHYPIDPFIHFSQSEIEVSVAIRNRLLSFOR 60
 DB 57 DOTATYIRMLGTVRVRAGFESERRGSHYPIDPFIHFSQSEIEVSVAIRNRLLSFOR 116
 QY 61 YLRSSRFRTAVSNSNIILDDYNGQAKMCKGVGNWDFILFDRLTNGNSIVSLTEH 120
 DB 117 YLRSSRFRTAVSNSNIILDDYNGQAKMCKGVGNWDFILFDRLTNGNSIVSLTEH 176
 QY 121 LFSHGILIEVFLHDMKRLRFLVMQEDYHSONPYHNAVHAADVTQAMCYLKEPKPLANS 180
 DB 177 LFSHGILIEVFLHDMKRLRFLVMQEDYHSONPYHNAVHAADVTQAMCYLKEPKPLANS 236
 QY 181 VTPWDILLSIAAATHDLDHFGVGNQPFILKTNHYLATLYKNTSVLENHNRSAVGLLRES 240
 DB 237 VTPWDILLSIAAATHDLDHFGVGNQPFILKTNHYLATLYKNTSVLENHNRSAVGLLRES 296
 QY 241 GLFSLHPLFESRQOMETQIGALLIATDISRQNEYLSLFRSHLDRGDLCLEDFRHHVLMQ 300
 DB 297 GLFSLHPLFESRQOMETQIGALLIATDISRQNEYLSLFRSHLDRGDLCLEDFRHHVLMQ 356

QY 301 ALKCADICNPCKTWELSKQWSEKVTTEFFHQDIEKKYHLGVSPCLDRHTESIANIQIGF 360
 DB 357 ALKCADICNPCKTWELSKQWSEKVTTEFFHQDIEKKYHLGVSPCLDRHTESIANIQIGF 416
 QY 361 MTYLVEPLFTTEWARFNSNRLSQTMLGHVGLNKASWKGLOREQSSSEDTDAAFELNSQLLP 420
 DB 417 MTYLVEPLFTTEWARFNSNRLSQTMLGHVGLNKASWKGLOREQSSSEDTDAAFELNSQLLP 476
 QY 421 QENRLS 426
 DB 477 QENRLS 482
 RESULT 4
 AAW00094
 ID AAW00094 standard; protein; 498 AA.
 XX AC AAW00094;
 XX 25-MAR-2003 (revised)
 DT 09-OCT-1996 (first entry)
 XX CAMP phosphodiesterase encoded by plasmid pTM22 (ATCC 68601).
 DE Human; glioblastoma cell; heat shock sensitivity; phosphodiesterase;
 KW deficient yeast strain 10DAB; pTM22; rat DPD phosphodiesterase; pdel-;
 KW bovine Ca2+/calmodulin dependent cAMP phosphodiesterase; heart; plasmid;
 KW RAS2(val19); pde2-; pTM3; pTM72; pRATDPD; pJC99; rolipram sensitive.
 XX Homo sapiens.
 OS US5527896-A.
 PN 18-JUN-1996.
 PD 19-APR-1991; 91US-00688352.
 PF 20-APR-1990; 90US-00511715.
 PR (COLD-) COLD SPRING HARBOR LAB.
 XX Colicelli JJ, Wigler MH;
 WPI; 1996-299902/30.
 N-PSDB; AAT34376.
 PT DNA mols. isolated from human glioblastoma cells - encode RAS-related or
 PT cyclic nucleotide phosphodiesterase proteins.
 XX Claim 4; Col 67-70; 101pp; English.
 PS The sequences given in AAW00092-94 are encoded by plasmid fragments which
 CC contain human glioblastoma cell cDNA inserts which are capable of
 CC correcting the heat shock sensitivity of the phosphodiesterase deficient
 CC yeast strain 10DAB. Several cDNA's were isolated and sequenced. pTM22
 CC encodes a novel human gene. From computer analysis, pTM22 putatively
 CC encodes a protein homologous to various cAMP phosphodiesterases, such as
 CC the bovine Ca2+/calmodulin dependent cAMP phosphodiesterase and the rat
 CC DPD phosphodiesterase. Sequences related to pTM22 were found to be
 CC expressed in human heart. Plasmid pTM22 was unable to correct the heat
 CC shock sensitivity of RAS2(val19) yeast strains. It thus appears that the
 CC pdel- and pde2- yeast strain 10DAB is more sensitive to phenotypic
 CC reversion by mammalian cAMP phosphodiesterase clones than is the
 CC RAS2(val19) yeast strain. The inserts in the plasmids pTM3 and pTM72 were
 CC also characterized. These two different cAMP phosphodiesterase cDNA's
 CC were found to be closely related to, but distinct from, the pRATDPD
 CC insert and the pJC99 insert. Biochemical analysis of cell lysates has
 CC established that the cDNA's of pTM3 and pTM72, pJC44x and pRATDPD encode
 CC rolipram sensitive cAMP phosphodiesterases. (Updated on 25-MAR-2003 to
 CC correct PF field.)
 XX Sequence 498 AA;

Query Match	100.0%;	Score 2243;	DB 2;	Length 498;
Best Local Similarity	100.0%;	Pred. NO. 8.1e-226;	Indels	0; Gaps 0;
Matches 426;	Conservative	0; Mismatches	0;	
QY	1	DQTALYIRMLGDVVRSRAGFESERRGSHPIYDFRIHFSQSEIEVSVSARNIRLLSFQR	60	
DB	73	DQTALYIRMLGDVVRSRAGFESERRGSHPIYDFRIHFSQSEIEVSVSARNIRLLSFQR	132	
QY	61	YLRSRPFRTAVSNSINILDDYNGQAKCMLEKVGWNVEDIFLFDRLTNGNSLVSLTFH	120	
DB	133	YLRSRPFRTAVSNSINILDDYNGQAKCMLEKVGWNVEDIFLFDRLTNGNSLVSLTFH	192	
QY	121	LFSLHGILIEYFHLDMKLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS	180	
DB	193	LFSLHGILIEYFHLDMKLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS	252	
QY	181	VTPWDIILLSLIAAATHDLDHPGVNQPFLLIKTNHYLATLYKNTSVLENHHWRSVAGLLRES	240	
DB	253	VTPWDIILLSLIAAATHDLDHPGVNQPFLLIKTNHYLATLYKNTSVLENHHWRSVAGLLRES	312	
QY	241	GLFSHLPLESRQOMETQIGALILATDISRQNEYLSLFESHLDRGDLCEDTFRHRLVLQM	300	
DB	313	GLFSHLPLESRQOMETQIGALILATDISRQNEYLSLFESHLDRGDLCEDTFRHRLVLQM	372	
QY	301	ALKCADICNPCRTWELSKQWSEKVTETEEFFHOGDIEKKYHLGVSPICDRHTESIANIQIGF	360	
DB	373	ALKCADICNPCRTWELSKQWSEKVTETEEFFHOGDIEKKYHLGVSPICDRHTESIANIQIGF	432	
QY	361	MTYLVEPLFTFEWARFSNTRLQSOTMLGHVGLNKASWKGLQREQSSSEDTDAAPFELNSQLLP	420	
DB	433	MTYLVEPLFTFEWARFSNTRLQSOTMLGHVGLNKASWKGLQREQSSSEDTDAAPFELNSQLLP	492	
QY	421	QENRLS 426		
DB	493	QENRLS 498		
RESULT 5				
AAAY49808				
ID	AAAY49808	standard; protein; 498 AA.		
AC	AAAY49808;			
DT				
DE	19-JAN-2000 (first entry)			
KW	Human glioblastoma cell CAMP phosphodiesterase pTM22 protein.			
KW	Phosphodiesterase; dunce-like phosphodiesterase; PDB; DPD; CAMP;			
KW	RAS-related protein; immunoreactive; detection; genetic defect;			
KW	bronchodilation; increased myocardial contractility; anti-inflammation.			
OS	Homo sapiens.			
PN	US5977305-A.			
PD	02-NOV-1999.			
PF	07-JUN-1995; 95US-00474379.			
PR	20-APR-1990; 90US-00511715.			
PR	19-APR-1991; 91US-00688352.			
PR	01-MAR-1994; 94US-00206188.			
XX	(COLD-) COLD SPRING HARBOR LAB.			
XX	Colicelli JJ, Wigler MH;			
XX	WPI; 1999-619709/53.			
XX	N-PSDB; AA232240.			
XX	New isolated RAS-related polypeptides and mammalian cyclic nucleotide			
XX	phosphodiesterases, used for screening for agents which can modify			
XX	phenomenon or suppress genetic defects.			

OS Saccharomyces cerevisiae.
 XX US6100025-A.
 XX PD 08-AUG-2000.
 XX PF 01-MAR-1994; 9AUS-00206188.
 XX PR 20-APR-1990; 9OUS-00511715.
 XX PR 19-APR-1991; 9IUS-00688352.
 XX PA (COLD-) COLD SPRING HARBOR LAB.
 XX PI Colicelli JJ, Wigler MH;
 XX DR WPI; 2000-531664/48.
 XX DR N-PSDB; AAA88175.
 XX PT Novel isolated DNA encoding a mammalian cyclic nucleotide
 PT phosphodiesterase is present in plasmids pPDE46, pPDE43 or pPDE339 and is
 PT used to modify a genetic defect in a biochemical pathway in which cAMP
 PT participates.
 XX PS Example 1; Col 85-88; 145pp; English.
 XX CC The present invention describes a purified and isolated DNA (I) which
 CC encodes a mammalian cyclic nucleotide phosphodiesterase and is an insert
 CC present in the plasmids pPDE46 (ATCC 69552), pPDE43 (ATCC 69551) or
 CC pPDE339 (ATCC 69550). The DNA molecules are used to modify, complement or
 CC suppress a genetic defect in a biochemical pathway in which cAMP
 CC participates and are also used as hybridisation probes. The present
 CC invention also describes methods for detecting mammalian genes encoding
 CC proteins which can function in microorganisms, particularly yeast, to
 CC modify, complement, or suppress a genetic defect associated with an
 CC identifiable phenotypic alteration or characteristic in the
 CC microorganism. AAA88162 to AAA88218 and AAB29614 to AAB20640 represent
 CC sequences used in the exemplification of the present invention
 XX Sequence 498 AA;
 SQ Query Match 100.0%; Score 2243; DB 3; Length 498;
 Best Local Similarity 100.0%; Pred. No. 8.1e-226;
 Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DOTALYIRMLGDVVRSGAGFESERRGSHPIYDIPRPHSOSEIEVSASRNIRLLSFQR 60
 DB 73 DQALYIRMLGDVVRSGAGFESERRGSHPIYDIPRPHSOSEIEVSASRNIRLLSFQR 132
 QY 61 YLRSSRRFRGTAVSNSNILDYNGQAKCMLEKVGNNWDFIFLFDRLTNGNSLVSTFH 120
 DB 133 YLRSSRRFRGTAVSNSNILDYNGQAKCMLEKVGNNWDFIFLFDRLTNGNSLVSTFH 192
 QY 121 LFSHLGLIEFHLDMKRLRFLVMQEDYISQNPYHNAVAADVTQAMHCYKPEKPLANS 180
 DB 193 LFSHLGLIEFHLDMKRLRFLVMQEDYISQNPYHNAVAADVTQAMHCYKPEKPLANS 252
 QY 181 VTPWDILSLIAAATHDLDPGVNPPFLIKTNHVLATLYKNTSVLENHHRWSAVGLLRES 240
 DB 253 VTPWDILSLIAAATHDLDPGVNPPFLIKTNHVLATLYKNTSVLENHHRWSAVGLLRES 312
 QY 241 GLFHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDCLIEDTRHRLVLQM 300
 DB 313 GLFHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDCLIEDTRHRLVLQM 372
 QY 301 ALKCADICNPRTWELSKQWEKTEEPFHQGDIEKKYHLGVSLCDRHTESIANIQIGF 360
 DB 373 ALKCADICNPRTWELSKQWEKTEEPFHQGDIEKKYHLGVSLCDRHTESIANIQIGF 432
 QY 361 MTYLVEPLFTWAFSNTRLSQTMLGHVGLNKAWSKGLQREQSSSEDTAAPFELSOLLP 420
 DB 433 MTYLVEPLFTWAFSNTRLSQTMLGHVGLNKAWSKGLQREQSSSEDTAAPFELSOLLP 492
 QY 421 QENRLS 426

Db 493 QENRLS 498
 |||||
 RESULT 7
 ID AAE24529
 XX AAE24529 standard; protein; 426 AA.
 AC AAE24529;
 XX 04-OCT-2002 (first entry)
 DT Rat PDE7 protein.
 DE Phosphodiesterase 7; PDE7; AIDS; acquired immune deficiency syndrome;
 XX immune system disease; enzyme; chronic obstructive pulmonary disease;
 KW T-cell related disease; autoimmune disorder; Crohn's disease; cancer;
 KW rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
 KW colitis; COPD; asthma; therapy; rat.
 XX Rattus sp.
 OS WO200226954-A2.
 XX 04-APR-2002.
 PD 28-SEP-2001; 2001WO-EP011303.
 XX 28-SEP-2000; 2000EP-00402683.
 PR (WARN) WARNER LAMBERT CO.
 PA Souland P;
 XX WPI; 2002-479561/51.
 DR N-PSDB; AAB39378.
 XX Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity
 PT than endogenous full length PDE7, for screening of PDE7 inhibitors useful
 PT in preventing and treating autoimmune disorders and inflammatory
 PT diseases.
 XX Claim 2; Page 127-128; 137pp; English.
 PS The invention relates to novel polypeptides exhibiting a higher
 CC phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length
 CC PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of
 CC the invention are used for screening compounds that inhibit PDE7
 CC activity. PDE7 inhibitors are used for manufacturing a pharmaceutical
 CC composition useful for the treatment or prevention of various
 CC pathological conditions such as diseases affecting the immune system,
 CC including acquired immune deficiency syndrome (AIDS), rejection of
 CC transplant, autoimmune disorders such as T-cells related diseases for
 CC e.g. rheumatoid arthritis, inflammatory diseases such as respiratory
 CC inflammation diseases including chronic obstructive pulmonary disease
 CC (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's
 CC disease, colitis, pancreatitis and different types of cancers including
 CC leukaemia. The present sequence is rat PDE7 protein
 XX Sequence 426 AA;
 SQ Query Match 94.3%; Score 2116; DB 5; Length 426;
 Best Local Similarity 94.1%; Pred. No. 1.3e-212;
 Matches 401; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
 QY 1 DOTALYIRMLGDVVRSGAGFESERRGSHPIYDIPRPHSOSEIEVSASRNIRLLSFQR 60
 DB 1 DOTALYIRMLGDVVRSGAGFESERRGSHPIYDIPRPHSOSEIEVSASRNIRLLSFQR 60
 QY 61 YLRSSRRFRGTAVSNSNILDYNGQAKCMLEKVGNNWDFIFLFDRLTNGNSLVSTFH 120
 DB 61 YLRSSRRFRGTAVSNSNILDYNGQAKCMLEKVGNNWDFIFLFDRLTNGNSLVSTFH 120

121 LFSHGLIEYFHLDMKRLRFLVMIQEDYHSQNPYHNAVHAADVTOAMHCYLKEPKLANS 180
 121 LFSHGLIEYFHLDMKRLRFLVMIQEDYHSQNPYHNAVHAADVTOAMHCYLKEPKLANS 180
 181 VTPWDILLSIAAATHDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSVGLLRES 240
 181 VTPWDILLSIAAATHDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSVGLLRES 240
 241 GLFSLHPLSRQOMETOIGALILATDISRONEYLSPFRSHLDGDLCTEHRHVLQOM 300
 241 GLFSLHPLSRHWEAQIGALILATDISRONEYLSPFRSHLDGDLCTEHRHVLQOM 300
 301 ALKCADICNPCTWELSKQWSEKVTSEFFHQGDIEKKYHLGVSPCLDRHTESIANIQIGF 360
 301 ALKCADICNPCTWELSKQWSEKVTSEFFHQGDIEKKYHLGVSPCLDRHTESIANIQIGF 360
 361 MTYLVEPLFTWARFSTRLSQTMGLHVLNKAWSKGLQREOSSEDTDAAFELNSQLLP 420
 361 MTYLVEPLFTWARFSTRLSQTMGLHVLNKAWSKGLQREOSSEDTDAAFELNSQLLP 420
 421 QENRSL 426
 421 QENRSL 426

RESULT 8
 AAE24533
 ID AAE24533 standard; protein; 428 AA.
 XX AC AAE24533;
 XX DT 04-OCT-2002 (first entry)
 XX DE Rat PDE7a protein.
 XX KW Phosphodiesterase 7; PDE7a; AIDS; acquired immune deficiency syndrome;
 XX KW immune system disease; enzyme; chronic obstructive pulmonary disease;
 XX KW T-cell related disease; autoimmune disorder; Crohn's disease; cancer;
 XX KW rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
 XX KW colitis; COPD; asthma; therapy; rat.
 XX OS Rattus sp.
 XX PN WO200226954-A2.
 XX PD 04-APR-2002.
 XX PF 28-SEP-2001; 2001WO-EP011303.
 XX PR 28-SEP-2000; 2000EP-00402683.
 XX PA (WARN) WARNER LAMBERT CO.
 XX PI Soulard P;
 XX WPI; 2002-479561/51.
 Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity
 than endogenous full length PDE7, for screening of PDE7 inhibitors useful
 in preventing and treating autoimmune disorders and inflammatory
 diseases.
 Disclosure; Fig 1; 137pp; English.
 The invention relates to novel polypeptides exhibiting a higher
 phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length
 PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of
 the invention are used for screening compounds that inhibit PDE7
 activity. PDE7 inhibitors are used for manufacturing a pharmaceutical
 composition useful for the treatment or prevention of various
 pathological conditions such as diseases affecting the immune system,
 including acquired immune deficiency syndrome (AIDS), rejection of
 transplant, autoimmune disorders such as T-cells related diseases for

CC e.g. rheumatoid arthritis, inflammatory diseases such as respiratory
 CC inflammation diseases including chronic obstructive pulmonary disease
 CC (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's
 CC disease, colitis, pancreatitis and different types of cancers including
 CC leukaemia. The present sequence is rat PDE7a protein
 XX
 SQ Sequence 428 AA;
 Query Match 94.3%; Score 2116; DB 5; Length 428;
 Best Local Similarity 94.1%; Pred. No. 1.3e-212;
 Matches 401; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
 QY 1 DQVALYRMLGDVVRSRAGFESRGRSHPIYDFRIFHQSSEIEVSVAENIRLLSFQR 60
 DB 3 DQVALYRMLGDVVRSRAGFETERRGSHPIYDFRIFHQAQSEIEVSVAENIRLLSFQR 62
 QY 61 YLRSSRFRGTAVNSNLIIDDDYNGQAKCMLKGVGNWDFDIFDLRTNGNSLVSTFH 120
 DB 63 YLRSSRFRGTAVNSNLIIDDDYNGQAKCMLKGVGNWDFDIFDLRTNGNSLVSTFH 122
 QY 121 LFSHGLIEYFHLDMKRLRFLVMIQEDYHSQNPYHNAVHAADVTOAMHCYLKEPKLANS 180
 DB 123 LFSHGLIEYFHLDMKRLRFLVMIQEDYHSQNPYHNAVHAADVTOAMHCYLKEPKLANS 182
 QY 181 VTPWDILLSIAAATHDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSVGLLRES 240
 DB 183 VTPWDILLSIAAATHDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSVGLLRES 242
 QY 241 GLFSLHPLSRQOMETOIGALILATDISRONEYLSPFRSHLDGDLCTEHRHVLQOM 300
 DB 243 GLFSLHPLSRHWEAQIGALILATDISRONEYLSPFRSHLDGDLCTEHRHVLQOM 302
 QY 301 ALKCADICNPCTWELSKQWSEKVTSEFFHQGDIEKKYHLGVSPCLDRHTESIANIQIGF 360
 DB 303 ALKCADICNPCTWELSKQWSEKVTSEFFHQGDIEKKYHLGVSPCLDRHTESIANIQIGF 362
 QY 361 MTYLVEPLFTWARFSTRLSQTMGLHVLNKAWSKGLQREOSSEDTDAAFELNSQLLP 420
 DB 363 MTYLVEPLFTWARFSTRLSQTMGLHVLNKAWSKGLQREOSSEDTDAAFELNSQLLP 422
 QY 421 QENRSL 426
 DB 423 QENRSL 428

RESULT 9
 AAE24528
 ID AAE24528 standard; protein; 426 AA.
 XX AC AAE24528;
 XX DT 04-OCT-2002 (first entry)
 XX DE Mouse PDE7 protein.
 XX KW Phosphodiesterase 7; PDE7; AIDS; acquired immune deficiency syndrome;
 XX KW immune system disease; enzyme; chronic obstructive pulmonary disease;
 XX KW T-cell related disease; autoimmune disorder; Crohn's disease; cancer;
 XX KW rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
 XX KW colitis; COPD; asthma; therapy; mouse.
 XX OS Mus sp.
 XX PH Key Location/Qualifiers
 FT Misc-difference 23
 FT /note= "Encoded by TCA"
 FT Misc-difference 42
 FT /note= "Encoded by GAA"
 FT Misc-difference 45
 FT /note= "Encoded by GTG"
 FT Misc-difference 67
 FT /note= "Encoded by TTT"
 FT Misc-difference 71


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PR 28-SEP-2000; 2000EP-00402683.
XX (WARN ) WARNER LAMBERT CO.
XX Soulard P;
XX WPI; 2002-479561/51.
DR N-PSDB; AAD39383.
XX Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity
PT than endogenous full length PDE7, for screening of PDE7 inhibitors useful
PT in preventing and treating autoimmune disorders and inflammatory
PT diseases.
XX
XX Disclosure; Fig 1; 137pp; English.
XX
XX The invention relates to novel polypeptides exhibiting a higher
CC phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length
CC PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of
CC PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of
CC the invention are used for screening compounds that inhibit PDE7
CC activity. PDE7 inhibitors are used for manufacturing a pharmaceutical
CC composition useful for the treatment or prevention of various
CC pathological conditions such as diseases affecting the immune system,
CC including acquired immune deficiency syndrome (AIDS), rejection of
CC transplant, autoimmune disorders such as T-cells related diseases for
CC e.g. rheumatoid arthritis, inflammatory diseases such as respiratory
CC inflammation diseases including chronic obstructive pulmonary disease
CC (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's
CC disease, colitis, pancreatitis and different types of cancers including
CC leukaemia. The present sequence is mouse PDE7A2 protein
XX
XX Sequence 456 AA;
XX
XX Query Match 93.8%; Score 2105; DB 5; Length 456;
XX Best Local Similarity 93.7%; Pred. No. 2.1e-211;
XX Matches 399; Conservative 13; Mismatches 14; Indels 0; Gaps 0;
XX
QY 1 DOTALYHMLGDVVRVSRAGSESRGSHPYIDRFIFHSQSEIEVSARNIRLLSFQR 60
Db . . . . .
QY 31 DOTALYHMLGDVVRVSRAGSESRGSHPYIDRFIFHSQSDIEASVARNIRLLSFQR 90
Db . . . . .
QY 61 YLRSSRFRGTAVNSLMLDDYNGQAKCMLEKVGNNWFIDFLDRLTNGNSLVSLTFH 120
Db . . . . .
QY 91 YLRSSRFRGTAVNSLMLDDYNGQAKCMLEKVGNNWFIDFLDRLTNGNSLVSLTFH 150
Db . . . . .
QY 121 LFSHLGLIEYFHLDMKMLRRFLVMTQEDYHSONPHYNAVHAADVTQAMHCVLKPKLANS 180
Db . . . . .
QY 151 LFSHLGLIEYFHLDMKMLRRFLVMTQEDYHSONPHYNAVHAADVTQAMHCVLKPKLANS 210
Db . . . . .
QY 181 VTPWDILLSIAAATHDHPGVNQPEFLIKTNHYLATLYKNTSVLENHHRSAVGLLRES 240
Db . . . . .
QY 211 VTPWDILLSIAAATHDHPGVNQPEFLIKTNHYLATLYKNTSVLENHHRSAVGLLRES 270
Db . . . . .
QY 241 GLFSLHPLSRQOMETQIGALILATDGRQNEYLFLSRHLDGRDCLDTHRHVLVLMQ 300
Db . . . . .
QY 271 GLFSLHPLSRQOMETQIGALILATDGRQNEYLFLSRHLDGRDCLDTHRHVLVLMQ 330
Db . . . . .
QY 301 ALKCADICNPCTWELSKQWSEKVTPEEPHQGDIEKKYHLGVSPICDRHTESIANIQIGF 360
Db . . . . .
QY 331 ALKCADICNPCTWELSKQWSEKVTPEEPHQGDIEKKYHLGVSPICDRHTESIANIQIGF 390
Db . . . . .
QY 361 MYVLVEPLFTWARFNTSLRSTMLGHVGLNKAWSKGLQREOSSEDTDAAFELNSQLIP 420
Db . . . . .
QY 391 MYVLVEPLFTWARFNTSLRSTMLGHVGLNKAWSKGLQREOSSEDTDAAFELNSQLIP 450
Db . . . . .
QY 421 QENRLS 426
Db . . . . .
QY 451 QENRLS 456
Db . . . . .
XX
XX RESULT 11
XX AAU79727
XX ID AAU79727 standard; protein; 424 AA.

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XX AC AAU79727;
XX DT 15-JUL-2002 (first entry)
XX DE Human cyclic nucleotide phosphodiesterase, PDE8A variant #3.
XX KW Human; cyclic nucleotide phosphodiesterase; PDE; T-cell activation;
XX KW immune disorder; graft versus host disease; GVHD; T-cell lymphoma;
XX KW acute lymphoblastic leukaemia; autoimmune disease; arthritis;
XX KW insulin dependent diabetes mellitus; Crohn's disease; multiple sclerosis;
XX KW scleroderma; mixed connective tissue disease; PDE8A; enzyme; variant.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 417
XX FT /label= Unknown
XX FT /note= "Encoded by CAT. This residue is illegible in the
XX FT specification"
XX
XX WC200222661-A2.
XX
XX 21-MAR-2002.
XX
XX 12-SEP-2001; 2001WO-US028503.
XX
XX 12-SEP-2000; 2000US-0232445P.
XX
XX 12-OCT-2000; 2000US-0240500P.
XX
XX (BEAV/) BEAVO J A.
XX (SEEB/) SEEBECK T.
XX (SODE/) SODELING S H.
XX (RASC/) RASCON A.
XX (ZORA/) ZORAGHI R.
XX (KUNZ/) KUNZ S.
XX (GONG/) GONG K.
XX (GLAV/) GLAVAS N.
XX
XX Beavo JA, Seebek T, Soderling SH, Rascon A, Zoraghi R, Kunz S;
XX Gong K, Glavas N;
XX
XX WPI; 2002-339862/37.
XX N-PSDB; ABK48863.
XX
XX New cyclic nucleotide phosphodiesterase polypeptides such as PDE8A,
XX PDE7A3, TBPDE2A, TBPDE2B, TBPDE2C or TBPDE2E, that are involved in T cell
XX activation, useful for diagnosis and treatment of immune disorders.
XX
XX Example 9; Fig 35; 165pp; English.
XX
XX The present invention relates to the isolation of novel cyclic nucleotide
XX phosphodiesterase (PDE) proteins such as PDE8A, PDE7A3, TBPDE2A, TBPDE2B,
XX TBPDE2C or TBPDE2E, that are involved in T-cell activation or that are
XX from Trypanosoma brucei. An antibody that recognises a PDE is useful for
XX isolating a PDE protein from T-cells or a cultured T-cell line. A
XX molecule that recognises and binds PDE8A or PDE7A3M1 is useful for
XX inhibiting functional PDE8A- or PDE7A3-associated T-cell interaction, and
XX for inhibiting an immune system disease. PDE proteins and the
XX polynucleotide sequences encoding them are useful in the diagnosis and
XX treatment of immune disorders such as graft versus host disease (GVHD),
XX psoriasis, immune disorders associated with graft transplantation
XX rejection, T-cell lymphoma, T-cell acute lymphoblastic leukaemia, and
XX autoimmune diseases such as Hashimoto's thyroiditis, primary myxoedema,
XX Grave's disease, insulin dependent diabetes mellitus, pemphigus, Crohn's
XX disease, multiple sclerosis, ulcerative colitis, Sjogren's syndrome, present
XX arthritis, scleroderma, and mixed connective tissue disease. The present
XX sequence represents human PDE8A variant #3
XX
XX Sequence 424 AA;
XX
XX Query Match 85.2%; Score 1910; DB 5; Length 424;
XX Best Local Similarity 99.5%; Pred. No. 5.3e-191;
XX
XX

```

		Matches	362;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1	DOTALYIRMLG	DVRVRSRAGF	SESRGSHPYD	FRIFHSQSEI	VSARNIRLL	SFOR	60			
Db	57	DOTALYIRMLG	DVRVRSRAGF	SESRGSHPYD	FRIFHSQSEI	VSARNIRLL	SFOR	116			
QY	61	YLRSSRFFRG	TAVSNLSN	LDYNGQAK	CMLEKVGNN	NFDIFL	FDRLTNGNS	LSVSLTPH	120		
Db	117	YLRSSRFFRG	TAVSNLSN	LDYNGQAK	CMLEKVGNN	NFDIFL	FDRLTNGNS	LSVSLTPH	176		
QY	121	LPSLGLIEYF	HLDMKURFL	VMIOEDYH	SQNPYHNA	VHAADVTQ	AMECYLKEP	KPLANS	180		
Db	177	LPSLGLIEYF	HLDMKURFL	VMIOEDYH	SQNPYHNA	VHAADVTQ	AMECYLKEP	KPLANS	236		
QY	181	VTPWDILLS	IAAATHD	LHPGVNQ	PFLIKTNH	LYLATLVK	NTSVLENH	HWRSAGVLLRES	240		
Db	237	VTPWDILLS	IAAATHD	LHPGVNQ	PFLIKTNH	LYLATLVK	NTSVLENH	HWRSAGVLLRES	296		
QY	241	GLFSLPLESR	QMQETQIG	ALILATDIS	RQNEYSLS	FRSHLD	RGDICLED	TRRHHLVLQW	300		
Db	297	GLFSLPLESR	QMQETQIG	ALILATDIS	RQNEYSLS	FRSHLD	RGDICLED	TRRHHLVLQW	356		
QY	301	ALKACADICN	PCRTWELSK	QWSEKVTB	EPFHQGDIE	KYHLGVSP	LCDRHTES	IANIQIGF	360		
Db	357	ALKACADICN	PCRTWELSK	QWSEKVTB	EPFHQGDIE	KYHLGVSP	LCDRHTES	IANIQIGN	416		
QY	361	MTYL	364								
Db	417	XYTL	420								
RESULT 12											
ID	AAU16967										
XX	AAU16967; standard; protein; 432 AA.										
XX	07-NOV-2001 (first entry)										
DE	Human novel secreted protein, SEQ ID 208.										
KW	Human; immunosuppressive; antiarthritic; antiinflammatory; cytostatic;										
KW	cardiant; vasotropic; cerebroprotective; neurotropic; neuroprotective;										
KW	antibacterial; virucide; fungicide; ophthalmological; vulnerary;										
KW	secreted protein; rheumatoid arthritis; hyperproliferative disorder;										
KW	cardiovascular disorder; cardiac arrest; cerebrovascular disorder;										
KW	cerebral ischaemia; angiogenesis; nervous system disorder;										
KW	Alzheimer's disease; infection; ocular disorder; corneal infection;										
KW	wound healing; epithelial cell proliferation; skin ageing; food additive;										
XX	preservative; antiproliferative.										
OS	Homo sapiens.										
XX	WO200155441-A2.										
PD	02-AUG-2001.										
XX	17-JAN-2001; 2001WO-US001320.										
XX	31-JAN-2000; 2000US-0179065P.										
PR	04-FEB-2000; 2000US-0180628P.										
PR	24-FEB-2000; 2000US-0184664P.										
PR	02-MAR-2000; 2000US-0186350P.										
PR	16-MAR-2000; 2000US-0189874P.										
PR	17-MAR-2000; 2000US-0190076P.										
PR	18-APR-2000; 2000US-0198123P.										
PR	19-MAY-2000; 2000US-0205515P.										
PR	07-JUN-2000; 2000US-0209467P.										
PR	28-JUN-2000; 2000US-0214886P.										
PR	30-JUN-2000; 2000US-0215135P.										
PR	07-JUL-2000; 2000US-0216647P.										
PR	20-JUL-2000; 2000US-0216880P.										
PR	11-JUL-2000; 2000US-0217487P.										

PR	11-JUL-2000;	2000US-0217496P.
PR	14-JUL-2000;	2000US-0218290P.
PR	26-JUL-2000;	2000US-0220963P.
PR	26-JUL-2000;	2000US-0220964P.
PR	14-AUG-2000;	2000US-0224518P.
PR	14-AUG-2000;	2000US-0224519P.
PR	14-AUG-2000;	2000US-0225213P.
PR	14-AUG-2000;	2000US-0225214P.
PR	14-AUG-2000;	2000US-0225266P.
PR	14-AUG-2000;	2000US-0225267P.
PR	14-AUG-2000;	2000US-0225268P.
PR	14-AUG-2000;	2000US-0225270P.
PR	14-AUG-2000;	2000US-0225447P.
PR	14-AUG-2000;	2000US-0225757P.
PR	14-AUG-2000;	2000US-0225758P.
PR	14-AUG-2000;	2000US-0225759P.
PR	18-AUG-2000;	2000US-0226273P.
PR	22-AUG-2000;	2000US-0226681P.
PR	22-AUG-2000;	2000US-0226686P.
PR	22-AUG-2000;	2000US-0227182P.
PR	23-AUG-2000;	2000US-0227009P.
PR	30-AUG-2000;	2000US-0228924P.
PR	01-SEP-2000;	2000US-0229287P.
PR	01-SEP-2000;	2000US-0229343P.
PR	01-SEP-2000;	2000US-0229344P.
PR	01-SEP-2000;	2000US-0229345P.
PR	05-SEP-2000;	2000US-0229509P.
PR	05-SEP-2000;	2000US-0229513P.
PR	06-SEP-2000;	2000US-0230437P.
PR	06-SEP-2000;	2000US-0230438P.
PR	08-SEP-2000;	2000US-0231242P.
PR	08-SEP-2000;	2000US-0231243P.
PR	08-SEP-2000;	2000US-0231244P.
PR	08-SEP-2000;	2000US-0231413P.
PR	08-SEP-2000;	2000US-0231414P.
PR	08-SEP-2000;	2000US-0232080P.
PR	12-SEP-2000;	2000US-0231968P.
PR	14-SEP-2000;	2000US-0232397P.
PR	14-SEP-2000;	2000US-0232398P.
PR	14-SEP-2000;	2000US-0232399P.
PR	14-SEP-2000;	2000US-0232400P.
PR	14-SEP-2000;	2000US-0232401P.
PR	14-SEP-2000;	2000US-0233063P.
PR	14-SEP-2000;	2000US-0233064P.
PR	14-SEP-2000;	2000US-0233065P.
PR	21-SEP-2000;	2000US-0234223P.
PR	21-SEP-2000;	2000US-0234274P.
PR	25-SEP-2000;	2000US-0234997P.
PR	25-SEP-2000;	2000US-0234998P.
PR	26-SEP-2000;	2000US-0235484P.
PR	27-SEP-2000;	2000US-0235834P.
PR	27-SEP-2000;	2000US-0235836P.
PR	29-SEP-2000;	2000US-0236327P.
PR	29-SEP-2000;	2000US-0236367P.
PR	29-SEP-2000;	2000US-0236368P.
PR	29-SEP-2000;	2000US-0236370P.
PR	02-OCT-2000;	2000US-0236802P.
PR	02-OCT-2000;	2000US-0237037P.
PR	02-OCT-2000;	2000US-0237038P.
PR	02-OCT-2000;	2000US-0237039P.
PR	02-OCT-2000;	2000US-0237040P.
PR	13-OCT-2000;	2000US-0239935P.
PR	13-OCT-2000;	2000US-0239937P.
PR	20-OCT-2000;	2000US-0240960P.
PR	20-OCT-2000;	2000US-0241221P.
PR	20-OCT-2000;	2000US-0241785P.
PR	20-OCT-2000;	2000US-0241786P.
PR	20-OCT-2000;	2000US-0241787P.
PR	20-OCT-2000;	2000US-0241808P.
PR	20-OCT-2000;	2000US-0241809P.
PR	20-OCT-2000;	2000US-0241826P.

01-NOV-2000; 2000US-0244617P.
08-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246475P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246478P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246525P.
08-NOV-2000; 2000US-0246526P.
08-NOV-2000; 2000US-0246527P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246532P.
08-NOV-2000; 2000US-0246609P.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-0246613P.
17-NOV-2000; 2000US-0249207P.
17-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249209P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249212P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249215P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249217P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249245P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249299P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-0251988P.
05-DEC-2000; 2000US-0256719P.
06-DEC-2000; 2000US-0251479P.
08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251989P.
11-DEC-2000; 2000US-0251990P.
05-JAN-2001; 2001US-0259678P.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Baraah SC, Ruben SM;
WPI; 2001-476222/51.
N-PSDB; AAS26872.
Novel polypeptides and polynucleotides useful as diagnostic reagents to
diagnose diseases or disorders associated with aberrant expression or
activity of polypeptides, for treating blood clotting disorder,
hemophilia.
Claim 11; SEQ ID NO 208; 601pp; English.
The invention relates to isolated nucleic acid molecules and their
encoded secreted proteins. The nucleic acids and proteins are used to
prevent, treat or ameliorate a medical condition in e.g. humans, mice,
rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
in diagnosing a pathological condition or susceptibility to a
pathological condition. Antibodies to the proteins can also be used in
alleviating symptoms associated with the disorders and in diagnostic
immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays
(ELISA). Disorders which are diagnosed or treated include autoimmune

CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC and many other disorders listed in the specification. The polypeptides
CC can also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence represents a novel secreted protein of the invention. Note: The
Query Match 84.8%; Score 1903; DB 4; Length 432;
Best Local Similarity 99.2%; Pred. No. 3e-190;
Matches 361; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 DOTALYIRMLGADVVRVRAGFESERRGSHFYIDFRIFHSQSEIEVSVSARNIRLLSFQR 60
Db 65 DOTALYIRMLGADVVRVRAGFESERRGSHFYIDFRIFHSQSEIEVSVSARNIRLLSFQR 124
Qy 61 YLRSSRFRTAVNSNLILDDYNGQAKCMLEKVGNNFDFLFDRLTNGNSIVSLTFH 120
Db 125 YLRSSRFRTAVNSNLILDDYNGQAKCMLEKVGNNFDFLFDRLTNGNSIVSLTFH 184
Qy 121 LFSLHGLIEFYHLDMMKRLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
Db 185 LFSLHGLIEFYHLDMMKRLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 244
Qy 181 VTPMDILLSLIAAATHDHPGVNQPELIKTNHYLATLYKNTSVLENHWRSAVGLLRES 240
Db 245 VTPMDILLSLIAAATHDHPGVNQPELIKTNHYLATLYKNTSVLENHWRSAVGLLRES 304
Qy 241 GLFSHLPESRQOMETOIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTTRHHVLQM 300
Db 305 GLFSHLPESRQOMETOIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTTRHHVLQM 364
Qy 301 ALKCADICNPCTWELSKQWSEKVTTEFFHOGDIEKKYHLGVSPICDRHTESIANIQIGF 360
Db 365 ALKCADICNPCTWELSKQWSEKVTTEFFHOGDIEKKYHLGVSPICDRHTESIANIQIGF 424
Qy 361 MTYL 364
Db 425 YTYL 428
RESULT 13
ABB07912
ID ABB07912 standard; protein; 336 AA.
XX AC ABB07912;
XX DT 30-JUL-2002 (first entry)
XX DE Human PDE7a3 splice variant polypeptide.
XX KW Cyclic adenosine monophosphate; cAMP; cAMP phosphodiesterase type 7;
XX PDE7a3; splice variant; transgenic; cardiac; antiinflammatory;
XX antiallergic; antiasthmatic; antiinfertility; vaccine; enzyme.
XX OS Homo sapiens.
XX PN WO200183772-A1.
XX PD 08-NOV-2001.
XX PF 27-APR-2001; 2001WO-EP004785.
XX PR 28-APR-2000; 2000EP-00109267.
XX (MERE) MERCK PATENT GMBH.
PA

XX PI Kluxen F;
 XX DR WPI; 2002-034516/04.
 XX DR N-PSDB; ABL58391.
 XX PT New polypeptide of splice variant of cyclic adenosine monophosphate
 XX PT phosphodiesterase type 7 (PDE7A3). The polypeptide can be expressed by
 XX PT inducing immune response against diseases e.g. cardiovascular diseases
 XX PT and asthma.
 XX PS Claim 2; Page 33-36; 40pp; English.
 XX CC This represents a splice variant of cyclic adenosine monophosphate (cAMP)
 XX CC phosphodiesterase type 7 (PDE7A3). The polypeptide can be expressed by
 XX CC standard recombinant methodology. The PDE7A3 splice variant polypeptides
 XX CC and polynucleotides are useful for treating cardiovascular diseases,
 XX CC asthma, allergy, inflammatory diseases, fertility disorders and
 XX CC immunoregulator disorders. The polynucleotides are useful for producing
 XX CC transgenic animals, which include knock-in animals (in which an animal
 XX CC gene is replaced by human equivalent within the genome of the animal),
 XX CC useful in drug discovery process, for target validation. The PDE7A3
 XX CC splice variant polypeptides and polynucleotides are useful as vaccines
 XX CC for inducing an immunological response in a mammal
 XX SQ Sequence 336 AA;
 Query Match 79.7%; Score 1787; DB 5; Length 336;
 Best Local Similarity 100.0%; Pred. NO. 3e-178;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 91 MLEKVGWNPDIIFLDRLTNGNSLVSTFHLFSIHGLIEYFHLDMKLRFLYMIQDYH 150
 DB 1 MLEKVGWNPDIIFLDRLTNGNSLVSTFHLFSIHGLIEYFHLDMKLRFLYMIQDYH 60
 QY 151 SQPNYHNAHAADVTOAMHCYLKEPKLANSVTPWDILLSLIAAATHDHPGVNQPLIK 210
 DB 61 SQPNYHNAHAADVTOAMHCYLKEPKLANSVTPWDILLSLIAAATHDHPGVNQPLIK 120
 QY 211 TNHYLATLYKNTSVLENNHWRSAVGLLRSGLSHLPESRQMQETQIGALILATDISRQ 270
 DB 121 TNHYLATLYKNTSVLENNHWRSAVGLLRSGLSHLPESRQMQETQIGALILATDISRQ 180
 QY 271 NEVLSLFRSHLDGDLCELTRRHHLVLQALKKADICNPRTWELSKQSEKVTREFFH 330
 DB 181 NEVLSLFRSHLDGDLCELTRRHHLVLQALKKADICNPRTWELSKQSEKVTREFFH 240
 QY 331 QGDIEKKYHLGVSPCLCDRHTESIANIQIGFMTYLVEPLFTWARFNSNTRLSQTMGLGHVGL 390
 DB 241 QGDIEKKYHLGVSPCLCDRHTESIANIQIGFMTYLVEPLFTWARFNSNTRLSQTMGLGHVGL 300
 QY 391 NKASWKGLOREQSSSETDAAFELNSQLLPQENRLS 426
 DB 301 NKASWKGLOREQSSSETDAAFELNSQLLPQENRLS 336
 RESULT 14
 AAU79713
 ID AAU79713 standard; protein; 424 AA.
 AC AAU79713;
 XX AAU79713;
 XX 15-JUN-2002 (first entry)
 DT Human phosphodiesterase, PDE7A3 splice variant.
 XX Human; cyclic nucleotide phosphodiesterase; PDE; T-cell activation;
 XX immune disorder; graft versus host disease; GVHD; T-cell lymphoma;
 XX acute lymphoblastic leukaemia; autoimmune disease; arthritis;
 XX insulin dependent diabetes mellitus; Crohn's disease; multiple sclerosis;
 XX scleroderma; mixed connective tissue disease; PDE7A3; enzyme; variant.
 XX Homo sapiens.
 OS

XX PH Key Location/Qualifiers
 FT misc_feature 1..424 Unknown
 FT /label= "All residues represented by Xaa are illegible in
 FT /note= "the specification"
 XX PN WO200222661-A2.
 XX PD 21-MAR-2002.
 XX PF 12-SEP-2001; 2001WO-US028503.
 XX PR 12-SEP-2000; 2000US-0232445P.
 XX PR 12-OCT-2000; 2000US-0240500P.
 XX PA (BEAV/) BEAVO J A.
 XX PA (SEEB/) SEEBECK T.
 XX PA (SODE/) SODERLING S H.
 XX PA (RASC/) RASCON A.
 XX PA (ZORA/) ZORAGHI R.
 XX PA (KUNZ/) KUNZ S.
 XX PA (GONG/) GONG K.
 XX PA (GLAV/) GLAVAS N.
 XX PI Beavo JA, Seebeck T, Soderling SH, Rascon A, Zoraghi R, Kunz S;
 PI Gong K, Glavas N;
 XX WPI; 2002-339862/37.
 XX New cyclic nucleotide phosphodiesterase polypeptides such as PDE8A,
 PT PDE7A3, TBPDE2B, TBPDE2C or TBPDE2E, that are involved in T cell
 PT activation, useful for diagnosis and treatment of immune disorders.
 XX Claim 2; Fig 8B; 165pp; English.
 XX The present invention relates to the isolation of novel cyclic nucleotide
 CC phosphodiesterase (PDE) proteins such as PDE8A, PDE7A3, TBPDE2A, TBPDE2B,
 CC TBPDE2C or TBPDE2E, that are involved in T-cell activation or that are
 CC from Trypanosoma brucei. An antibody that recognises a PDE is useful for
 CC isolating a PDE protein from T-cells or a cultured T-cell line. A
 CC molecule that recognises and binds PDE8A or PDE7A3MI is useful for
 CC inhibiting functional PDE8A- or PDE7A3-associated T-cell interaction, and
 CC for inhibiting an immune system disease. PDE proteins and the
 CC polynucleotide sequences encoding them are useful in the diagnosis and
 CC treatment of immune disorders such as graft versus host disease (GVHD),
 CC psoriasis, immune disorders associated with graft transplantation
 CC rejection, T-cell lymphoma, T-cell acute lymphoblastic leukaemia, and
 CC autoimmune diseases such as Hashimoto's thyroiditis, primary myxoedema,
 CC Grave's disease, insulin dependent diabetes mellitus, pemphigus, Crohn's
 CC disease, multiple sclerosis, ulcerative colitis, Sjogren's syndrome,
 CC arthritis, scleroderma, and mixed connective tissue disease. The present
 CC sequence represents human PDE7A3 splice variant. Note: The present
 CC sequence should be encoded by ABK4831. However, since the present
 CC sequence is of poor quality in the specification many of the residues are
 CC illegible
 XX SQ Sequence 424 AA;
 Query Match 76.5%; Score 1717; DB 5; Length 424;
 Best Local Similarity 92.0%; Pred. No. 9.4e-171;
 Matches 335; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 QY 1 DOTATYIRMLGDIYVRSGAGFESERRGSHPIYDFRIFHSQSEIEVSVSARNIRLLISFOR 60
 DB 57 DOTATYIRMLGDIYVRSGAGFESERRGSHPIYDFRIFHSQSEIEVSVSARNIRLLISFOR 116
 QY 61 YLRSSRFRGTAVSNSNILLDDYNGQAKMELKVGWNNFDFLFLRTNGNSLVSTFH 120
 DB 117 YLRSSRFRGTAVSNSNILLDDYNGQAKMELKVGWNNFDFLFLRTNGNSLVSTFH 176
 QY 121 LFSHGLIEYFHLDMKLRFLYMIQDYHSONPYHNAHAADVTOAMHCYLKEPKLANS 180

Db 177 LXLHGLIEYFHLDMKRLRFLVMIQEDYHSONPYHKAHVADVTQAXHCYCKEPLKXNS 236
 QY 181 VTPWDILLSLIAAATHDHPGVNQPLIKTNHYLATLYKNTSVLENHHRWSAVGLLRES 240
 Db 237 VXXKDILLSLIAAATHDHPGVNQPLIKTNHYLATLYKNTSVLENHHRWSAVGLLRES 296
 QY 241 GLFSLPLESRQOMETOIGALILATDISRQNEVLSLFRSHLDGRDGLCLEDTRHRHLVLQM 300
 Db 297 GLFSLPLESRQOMETOIGALILATDISRQNEVLSLFRSHLDGRDGLCLEDTRHRHLVLQM 356
 QY 301 ALKACDTCNCRWTWELSKQSEKVTBFFHQGDIEKKYHGVSPLCDRHTESIANIQIGF 360
 Db 357 ALKACDTCNCRWTWELSKQSEKVTBFFHQGDIEKKYHGVSPLCDRHTESIANIQIGF 416
 QY 361 MTYL 364
 Db 417 YXYL 420

RESULT 15

AAI93569
 ID AAY93569 standard; protein; 450 AA.

XX AC AAY93569;

XX DT 25-SEP-2000 (first entry)

XX DE Amino acid sequence of a human phosphodiesterase enzyme.

XX KW Phosphodiesterase; PDE-XIV; human; enzyme.

XX OS Homo sapiens.

XX PN EP1018559-A1.

XX PD 12-JUL-2000.

XX PF 09-NOV-1999; 99EP-00308902.

XX PR 23-DEC-1998; 98GB-00028603.

XX PR 17-SEP-1999; 99GB-00022123.

XX PA (PFIZ) PFIZER LTD.

XX PA (PFIZ) PFIZER INC.

XX PI Fidock M;

XX DR WPI; 2000-433274/38.

XX DR N-PSDB; AAA46651.

XX PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity.

XX PS Disclosure; Page 45-47; 104pp; English.

XX CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-

CC XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA))
 XX
 SQ Sequence 450 AA;
 Query Match 62.6%; Score 1403.5; DB 3; Length 450;
 Best Local Similarity 62.6%; Pred. No. 7.9e-138;
 Matches 258; Conservative 66; Mismatches 87; Indels 1; Gaps 1;
 QY 1 DQALYIRMLGDVVRVSRAFGESRSGSHPYIDFRIFHSQSEIEVSVAARNIRLLSFOR 60
 Db 18 DQNAKVCVCMGLDRLRGQTGVRAERGSYPFIDFRLLNSTTYSGETGKTKKVKRLLSFOR 77
 QY 61 YLSSRFFRGTAVSNSNLDDDDYNGOAKCMKGVGNWNPDIIFDLRLTNGNSLVLTCH 120
 Db 78 YFHASRLRLGIIPOAPLHLLDEDYLGQARHMLSKVGMWDFDIIFDLRLTNGNSLVLTCH 137
 QY 121 LFSLHGLIEYFHLDMKRLRFLVMIQEDYHSONPYHKAHVADVTQAXHCYCKEPLKXNS 180
 Db 138 LFNTHGLIHHFKLDVMTLHRFLVWQEDYHSONPYHKAHVADVTQAXHCYCKEPLKXNS 197
 QY 181 VTPWDILLSLIAAATHDHPGVNQPLIKTNHYLATLYKNTSVLENHHRWSAVGLLRES 240
 Db 198 LTPDLIMLGLTAAAHVDVHPGVNQPLIKTNHHLANLYONMSVLENHHRWSAVGLLRES 257
 QY 241 GLFSLPLESRQOMETOIGALILATDISRQNEVLSLFRSHLDGRDGLCLEDTRHRHLVLQM 300
 Db 258 RLLAHLEPKENTQDIEQOLGSLILATDINRQNEFLTRKLAHLNKLRLLEDAQDRHFLMQI 317
 QY 301 ALKACDTCNCRWTWELSKQSEKVTBFFHQGDIEKKYHGVSPLCDRHTESIANIQIGF 360
 Db 318 ALKACDTCNCRWTWELSKQSEKVTBFFHQGDIEKKYHGVSPLCDRHTESIANIQIGF 377
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 Db 378 MSYIVEPLFREWAFHTGNTLSENNLGHLANHQAQWKSLLPRQHRSGSGS 429

Search completed: May 26, 2004, 09:28:27
 Job time : 99 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2004, 09:24:28 ; Search time 23 Seconds
(without alignments)
956.203 Million cell updates/sec

Title: US-09-966-781A-1
Perfect score: 2243
Sequence: 1 DGTALYIRMLGDRVRSRAG.....DTDAAFELNSQLLPQENRLS 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A COMB.pap.*
2: /cgn2_6/prodata/2/iaa/5B COMB.pap.*
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6: /cgn2_6/prodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2243	100.0	498	1	US-07-688-352C-20
2	2243	100.0	498	2	US-08-474-379C-20
3	2243	100.0	498	3	US-09-146-249A-20
4	2243	100.0	498	3	US-08-206-188B-20
5	1383.5	61.7	502	3	US-09-330-970-1
6	871	38.8	320	3	US-09-330-970-3
7	555	24.7	610	2	US-08-974-565C-9
8	555	24.7	610	3	US-09-255-748-9
9	550	24.5	562	1	US-07-688-352C-4
10	550	24.5	562	2	US-08-942-521B-8
11	550	24.5	562	2	US-08-474-379C-4
12	550	24.5	562	3	US-09-146-249A-4
13	550	24.5	562	3	US-08-206-188B-4
14	550	24.5	562	5	PCT-US91-02714-4
15	550	24.5	564	2	US-08-942-521B-2
16	550	24.5	564	2	US-08-474-379C-59
17	550	24.5	564	3	US-09-146-249A-59
18	550	24.5	564	3	US-08-206-188B-59
19	550	24.5	564	3	US-09-192-702-2
20	550	24.5	564	4	US-08-445-474-2
21	550	24.5	564	5	PCT-US94-02612-2
22	550	24.5	736	1	US-07-688-352C-24
23	550	24.5	736	2	US-08-474-379C-24
24	550	24.5	736	3	US-09-146-249A-24
25	550	24.5	736	3	US-08-206-188B-24
26	550	24.5	736	5	PCT-US91-02714-23
27	549	24.5	564	2	US-08-577-492-34

28	549	24.5	564	3	US-09-079-630-34	Sequence 34, Appl
29	548.5	24.5	610	2	US-08-942-521B-7	Sequence 7, Appl
30	545	24.3	481	1	US-08-286-856C-2	Sequence 2, Appl
31	545	24.3	481	1	US-08-472-831-2	Sequence 2, Appl
32	545	24.3	506	1	US-08-286-856C-3	Sequence 3, Appl
33	545	24.3	506	1	US-08-472-831-3	Sequence 3, Appl
34	545	24.3	606	2	US-08-577-492-32	Sequence 32, Appl
35	545	24.3	606	2	US-09-079-630-32	Sequence 32, Appl
36	543	24.2	501	2	US-08-577-492-40	Sequence 40, Appl
37	543	24.2	501	2	US-09-079-630-40	Sequence 40, Appl
38	542	24.2	517	4	US-08-472-600-6	Sequence 6, Appl
39	542	24.2	517	4	US-09-717-953-6	Sequence 6, Appl
40	542	24.2	518	4	US-09-602-735B-2	Sequence 2, Appl
41	542	24.2	564	4	US-08-472-600-5	Sequence 5, Appl
42	542	24.2	564	4	US-09-717-953-5	Sequence 5, Appl
43	542	24.2	673	2	US-08-577-492-35	Sequence 35, Appl
44	542	24.2	673	2	US-08-474-379C-63	Sequence 63, Appl
45	542	24.2	673	3	US-09-146-249A-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1
US-07-688-352C-20
; Sequence 20, Application US/07688352C
; Patent No. 5527896
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John H.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/688,352C
; FILING DATE: 19910419
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 27805/30197
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 984-9740
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-688-352C-20

Query Match 100.0%; Score 2243; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. NO. 5.4e-232;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQALYIRMLGDVVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVARNIRRLISFOR 60
DB 73 DQALYIRMLGDVVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVARNIRRLISFOR 132
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DB 133 YLRSSRRFRGTAVSNSINILDDDDYNGQAKCMLEKVGNNWFDIFLFDRLTNGNSLVSLTFH 192
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DB 193 LFSHGLIEYFHLDDMKLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 252
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DB 253 VTPWDILLSLIAAATHDHPGVNPPFLIKTNHYLATLYKNTSVLENHHRSAVGLLRES 312
QY 241 GLFSHLPLESRRQOMETQIGALILATDISRQNEVLSLFRSHLDRGDLCLEDTTRHRLVLM 300
DB 313 GLFSHLPLESRRQOMETQIGALILATDISRQNEVLSLFRSHLDRGDLCLEDTTRHRLVLM 372
QY 301 ALKADICNPCTRWELSKWSEKVTBEEFFHQGDIEKKYHGVSPCLCDRHTESIANIQIF 360
DB 373 ALKADICNPCTRWELSKWSEKVTBEEFFHQGDIEKKYHGVSPCLCDRHTESIANIQIF 432
QY 361 MTYLVEPLFTWARFSNTRLSQTMGLHVGLNKASWKGLOEQSSSETDAAAFELNSQLLP 420
DB 433 MTYLVEPLFTWARFSNTRLSQTMGLHVGLNKASWKGLOEQSSSETDAAAFELNSQLLP 492
QY 421 QENRLS 426
DB 493 QENRLS 498

RESULT 2

US-08-474-379C-20
; Sequence 20, Application US/08474379C
; Patent No. 5977305
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
; TITLE OF INVENTION: PROCESSES
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,379C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/206,188
; FILING DATE: 01-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,352
; FILING DATE: 19-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 27866/32771

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-379C-20

Query Match 100.0%; Score 2243; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 5.4e-232;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQALYIRMLGDVVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVARNIRRLISFOR 60
DB 73 DQALYIRMLGDVVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVARNIRRLISFOR 132
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DB 133 YLRSSRRFRGTAVSNSINILDDDDYNGQAKCMLEKVGNNWFDIFLFDRLTNGNSLVSLTFH 192
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DB 193 LFSHGLIEYFHLDDMKLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 252
QY 181 VTPWDILLSLIAAATHDHPGVNPPFLIKTNHYLATLYKNTSVLENHHRSAVGLLRES 240
DB 253 VTPWDILLSLIAAATHDHPGVNPPFLIKTNHYLATLYKNTSVLENHHRSAVGLLRES 312
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QY 301 ALKADICNPCTRWELSKWSEKVTBEEFFHQGDIEKKYHGVSPCLCDRHTESIANIQIF 360
DB 373 ALKADICNPCTRWELSKWSEKVTBEEFFHQGDIEKKYHGVSPCLCDRHTESIANIQIF 432
QY 361 MTYLVEPLFTWARFSNTRLSQTMGLHVGLNKASWKGLOEQSSSETDAAAFELNSQLLP 420
DB 433 MTYLVEPLFTWARFSNTRLSQTMGLHVGLNKASWKGLOEQSSSETDAAAFELNSQLLP 492
QY 421 QENRLS 426
DB 493 QENRLS 498

RESULT 3

US-09-146-249A-20
; Sequence 20, Application US/09146249A
; Patent No. 6069240
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,249A
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-146-249A-20

Query Match      100.0%; Score 2243; DB 3; Length 498;
Best Local Similarity 100.0%; Pred. No. 5.4e-232;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 73 DOTALYIRMLGTVRSRAGFESERGGSHPYIDFRIFHSQSEIEVSVARNIRLLSFQR 132

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DB 253 VTPWDILLSIAAATHDLDHPGVNQPLIKTNHYLATLYKNTSVLENHHWRSVAGLLRES 312

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DB 313 GLFSLPLESRQOMETQIGALILATDISRQNEVLSLFRSHLDRGDLCLEDRHRHLVLM 372

QY 301 ALKCADI CNPCRTWELSKQWSEKVTTEFFHQGDIEKKYHGVSPLCDRHTESIANIQIGF 360
DB 373 ALKCADI CNPCRTWELSKQWSEKVTTEFFHQGDIEKKYHGVSPLCDRHTESIANIQIGF 432

QY 361 MTYLVEPLFTWARFNSNTRLSQTMGLGVGNKASWKGLOREQSSSEDTDAAFELNSQLLP 420
DB 433 MTYLVEPLFTWARFNSNTRLSQTMGLGVGNKASWKGLOREQSSSEDTDAAFELNSQLLP 492

QY 421 QENRLS 426
DB 493 QENRLS 498

RESULT 4
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; Sequence 20, Application US/08206188B
; Patent No. 6100025
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America

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; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,188B
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-206-188B-20

Query Match      100.0%; Score 2243; DB 3; Length 498;
Best Local Similarity 100.0%; Pred. No. 5.4e-232;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DOTALYIRMLGTVRSRAGFESERGGSHPYIDFRIFHSQSEIEVSVARNIRLLSFQR 60
DB 73 DOTALYIRMLGTVRSRAGFESERGGSHPYIDFRIFHSQSEIEVSVARNIRLLSFQR 132

QY 61 YLRSSRFFRGTA VNSNLNILLDDYNGQAKCMLEKVGNNWNPDIPLFDRLTNGNSLVSLTFH 120
DB 133 YLRSSRFFRGTA VNSNLNILLDDYNGQAKCMLEKVGNNWNPDIPLFDRLTNGNSLVSLTFH 192

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DB 193 LFSHLGLIEYFHLDMKLRFLVMIQEDYHSQNPYHNAHAAVDTQAMHCYLKEPKLANS 252

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DB 253 VTPWDILLSIAAATHDLDHPGVNQPLIKTNHYLATLYKNTSVLENHHWRSVAGLLRES 312

QY 241 GLFSLPLESRQOMETQIGALILATDISRQNEVLSLFRSHLDRGDLCLEDRHRHLVLM 300
DB 313 GLFSLPLESRQOMETQIGALILATDISRQNEVLSLFRSHLDRGDLCLEDRHRHLVLM 372

QY 301 ALKCADI CNPCRTWELSKQWSEKVTTEFFHQGDIEKKYHGVSPLCDRHTESIANIQIGF 360
DB 373 ALKCADI CNPCRTWELSKQWSEKVTTEFFHQGDIEKKYHGVSPLCDRHTESIANIQIGF 432

QY 361 MTYLVEPLFTWARFNSNTRLSQTMGLGVGNKASWKGLOREQSSSEDTDAAFELNSQLLP 420
DB 433 MTYLVEPLFTWARFNSNTRLSQTMGLGVGNKASWKGLOREQSSSEDTDAAFELNSQLLP 492

QY 421 QENRLS 426
DB 493 QENRLS 498

RESULT 5
US-09-330-970-1
; Sequence 1, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; APPLICANT: Kapeller-Libermann, Rosana

```


; APPLICANT: White, David
 ; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
 ; FILE OF INVENTION: Phosphodiesterase
 ; FILE REFERENCE: 5800-28
 ; CURRENT APPLICATION NUMBER: US/09/330,970
 ; CURRENT FILING DATE: 1999-06-11
 ; EARLIER APPLICATION NUMBER: 09/277,423
 ; EARLIER FILING DATE: 1999-03-26
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 502
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-330-970-1

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 Best Local Similarity 62.9%; Pred. No. 1.1e-139;
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 DB 80 GDRLRGQTVRAERRGSYPIDFRLLNSTTYSGEIGTKKKVKLLSFRIFASRLRG 139
 QY 71 TAVSNSINILDDYNGQAKMLEKVGNNWFDIFLFDRLTNGNSLVSLTFHLSHGLIEY 130
 DB 140 IIPQAPLHLLDEDYLGQARHMLSKVGWDFDIFLFDRLTNGNSLVTLCHLNFTHGLIHH 199
 QY 131 FHLDMKLRFLVMIOEDYHSQNPYHNAVAADVTQAMHCYKPKLANSVTPWDILLSL 190
 DB 200 FKLDVMVTLHRFLVMQVEDYHSQNPYHNAVAADVTQAMHCYKPKLASFLTPDIMLGL 259
 QY 191 IAAATHDLDPGVNQPFLIKTNHLYLATLYKNTSVLENHHRSAVGLRSGLSHLPLE 250
 DB 260 LAAAHVDVDPGVNQPFLIKTNHLLANLYQNMVLENHHRSTIGMRERLLAHLPKEM 319
 QY 251 RQOMETQIGALILATDISRQNYLSLFRSHLDRLDCLDTRHRLHVLQALKKADICNP 310
 DB 320 TDIEQLQGLSILATDINRQNEFLTRUKAHLNKKDLSDLEDAQDRHFMLQALKKADICNP 379
 QY 311 CRWELSKQWSEKVTFFHGGDIEKKYHLGVSPCLDRHTESIANIQIGMTYLVLEPLT 370
 DB 380 CRWELSKQWSEKVTFFHGGDIEKKYHLGVSPCLDRHTESIANIQIGMTYLVLEPLR 439
 QY 371 EWARFS-NTRLSTQMLGHVGLKASWKGLOREQSSSDTDA 411
 DB 440 EWARFTGNTSLSENMGLAHNAKQWKSLLPRQHRSGSGS 481

RESULT 6
 US-09-330-970-3
 ; Sequence 3, Application US/09330970
 ; Patent No. 6146876
 ; GENERAL INFORMATION:
 ; APPLICANT: Robison, Keith E.
 ; APPLICANT: Kapeller-Liberman, Rosana
 ; APPLICANT: White, David
 ; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
 ; FILE OF INVENTION: Phosphodiesterase
 ; FILE REFERENCE: 5800-28
 ; CURRENT APPLICATION NUMBER: US/09/330,970
 ; CURRENT FILING DATE: 1999-06-11
 ; EARLIER APPLICATION NUMBER: 09/277,423
 ; EARLIER FILING DATE: 1999-03-26
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-330-970-3

Query Match 38.8%; Score 871; DB 3; Length 320;

Best Local Similarity 66.9%; Pred. No. 6.1e-85;
 Matches 160; Conservative 34; Mismatches 45; Indels 0; Gaps 0;
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 QY 131 FHLDMKLRFLVMIOEDYHSQNPYHNAVAADVTQAMHCYKPKLANSVTPWDILLSL 190
 DB 200 FKLDVMVTLHRFLVMQVEDYHSQNPYHNAVAADVTQAMHCYKPKLASFLTPDIMLGL 259
 QY 191 IAAATHDLDPGVNQPFLIKTNHLYLATLYKNTSVLENHHRSAVGLRSGLSHLPLE 249
 DB 260 LAAAHVDVDPGVNQPFLIKTNHLLANLYQNMVLENHHRSTIGMRERLLAHLPKKE 318

RESULT 7
 US-08-974-565C-9
 ; Sequence 9, Application US/08974565C
 ; Patent No. 5932423
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Coleman, Roger
 ; APPLICANT: Seilhamer, Jeffrey J.
 ; APPLICANT: Fisher, Douglas A.
 ; TITLE OF INVENTION: CYCLIC NUCLEOTIDE PHOSPHODIESTERASES
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Dr.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/974,565C
 ; FILING DATE: Herewith
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/624,663
 ; FILING DATE: March 25, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murry, Lynn E.
 ; REGISTRATION NUMBER: 42,918
 ; REFERENCE/DOCKET NUMBER: PF-0057-1 CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 610 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 1705952
 US-08-974-565C-9

Query Match 24.7%; Score 555; DB 2; Length 610;
 Best Local Similarity 32.6%; Pred. No. 1.5e-50;
 Matches 127; Conservative 77; Mismatches 154; Indels 32; Gaps 7;

QY 8 RMLGDVVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSARNIRLLSFRQ----YLR 63

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Db 29 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNEVEIPSPTRQR---AFQOPPPSVLR 80
QY 64 SSR-----FFRGTA VNSLNI-----LDDYNGQAKCMLEKVGNNFDFILFRLTNG 111
Db 81 QSQPMQITGLKLVHTGSLNTNVPFRGVKTDQEDLLAQELENLKWLGNLFCVSEYAGG 140
QY 112 NSLVSITLPHLFSHLGLIEYFHLDMKLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCY 171
Db 141 RSLSCIMYTIQFORDLLKKFHPVDVTMMYMLTLEHDYHADVAYHNSLHAADVLOSTHYL 200
QY 172 LKEPKLANSVTWPDILLSLIAAATHDLDHPGVNQPELIKTNHYLATLYKNTSVLENHWR 231
Db 201 LATPALDAVFTDLEILAAALFAAAHVDVDPGVSNQFLINTSELALMYNDESLENHHLA 260
QY 232 SAVGLLRSG--LFSHLPLESQOMETQIGALILATDISRQNEYLSLFRSHLD-----R 283
Db 261 VGFKLQENECDFQNLKSRQRQSLRKMVIDMVLATDMSKHMTLLADLKTMTVETKVTSS 320
QY 284 GDLCLDTRHRLVLOMKALCADICNCPRTWELSKWSEKVTSEFFHOGDIEKKYHLGVS 343
Db 321 GVLLLDNYSDRIQVLRNMVHCADLSNPTKPELYRQWTDRIAMAEFFQOQDRERERGMEIS 380
QY 344 PLCDRHTESIANIQIGFMTYLYVEPLFTWA 373
Db 381 PWCXKHTASVEKSOVGFIDYIVHPLWETWA 410

RESULT 8
US-09-255-748-9
; Sequence 9, Application US/09255748
; Patent No. 6080548
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Coleman, Roger
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Fisher, Douglas A.
; TITLE OF INVENTION: CYCLIC NUCLEOTIDE PHOSPHODIESTERASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/255,748
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,565
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0057-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
```

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; CLONE: 1705952
US-09-255-748-9

Query Match 24.7%; Score 555; DB 3; Length 610;
Best Local Similarity 32.6%; Pred. No. 1.5e-50;
Matches 127; Conservative 77; Mismatches 154; Indels 32; Gaps 7;

QY 8 RMLGDVVRSRAGFSERSGSHPYIDFRIFHSQSELEVSVSARNIRLLSFQR----YLR 63
Db 29 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNEVEIPSPTRQR---AFQOPPPSVLR 80
QY 64 SSR-----FFRGTA VNSLNI-----LDDYNGQAKCMLEKVGNNFDFILFRLTNG 111
Db 81 QSQPMQITGLKLVHTGSLNTNVPFRGVKTDQEDLLAQELENLKWLGNLFCVSEYAGG 140
QY 112 NSLVSITLPHLFSHLGLIEYFHLDMKLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCY 171
Db 141 RSLSCIMYTIQFORDLLKKFHPVDVTMMYMLTLEHDYHADVAYHNSLHAADVLOSTHYL 200
QY 172 LKEPKLANSVTWPDILLSLIAAATHDLDHPGVNQPELIKTNHYLATLYKNTSVLENHWR 231
Db 201 LATPALDAVFTDLEILAAALFAAAHVDVDPGVSNQFLINTSELALMYNDESLENHHLA 260
QY 232 SAVGLLRSG--LFSHLPLESQOMETQIGALILATDISRQNEYLSLFRSHLD-----R 283
Db 261 VGFKLQENECDFQNLKSRQRQSLRKMVIDMVLATDMSKHMTLLADLKTMTVETKVTSS 320
QY 284 GDLCLDTRHRLVLOMKALCADICNCPRTWELSKWSEKVTSEFFHOGDIEKKYHLGVS 343
Db 321 GVLLLDNYSDRIQVLRNMVHCADLSNPTKPELYRQWTDRIAMAEFFQOQDRERERGMEIS 380
QY 344 PLCDRHTESIANIQIGFMTYLYVEPLFTWA 373
Db 381 PWCXKHTASVEKSOVGFIDYIVHPLWETWA 410

RESULT 9
US-07-688-352C-4
; Sequence 4, Application US/07688352C
; Patent No. 5527896
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/688,352C
; FILING DATE: 19910419
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 27805/30197
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
```

TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-688-352C-4

Query Match 24.5%; Score 550; DB 1; Length 562;
Best Local Similarity 31.8%; Pred. No. 4.5e-50;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

QY 8 RMLGDRVRVRAGFESERRGSHPIYDPRIFHSQSEIEVSVSARNIR-----LLSF 58
DB 82 RELTHLSEMSRSGNVSEYISNTFLD-----KQNDVEIPSPQDKREKKKKQQLMTQISG 136
QY 59 QRYLRSRFRFGTAVSN-SLNILDDYNGQAKCMLEKVGNNWDFILFDRLTNGNSLVSL 117
DB 137 VKLHMSSLNNTSISRGVNTENEDHLAKE---LEDLNKGLNIFNVAGYSHNRPLTCI 193
QY 118 TFLHLSLGLIEYFHLDMKRLRFLVMIQEDYHSONPYHNAVHAADVTQAMHCYKPEKL 177
DB 194 MYAIFQERDLKTKFISDFTVYMTLEHDYHSDVAYHNSLHAADVAQSTHLLSTPAL 253
QY 178 ANSVTPWDILLSLAAATHDLHPGVNQPFLIKTNHYLATLYKNTSVLENHHWSAVGLL 237
DB 254 DAVFTDLEILAAIFAAAHVDHPGVSNQFLINTNSLALMYNDESLENHHLAVGFKLL 313
QY 238 RES--GLFSLHPLESRQOMETQIGALILATDISRQNEYSLSFRSHLD-----RGDLCL 289
DB 314 QEEHCDIFQNLTKKQRTLRKVIDMVLATDMSKMSLLADLKTMTVETKVTSSGVLLLD 373
QY 290 DTRRHVLVQALMKACADICNCRTWELSKOWSEKVTBEFFHQDIEKKYHILGVSPICDRH 349
DB 374 NYTDRIQVLRNMVHCADLSNPTKSLEYLRQWTDRIEMBEFFQOGDKERERGMEISPMCDKH 433
QY 350 TESTANTQIGFTYVLEPLFTEWA 373
DB 434 TASVEKSGVGFIDYVHPLMETWA 457

RESULT 10
US-08-942-521B-8
Sequence 8, Application US/08942521B
Patent No. 5932477
GENERAL INFORMATION:
APPLICANT: Livi, George P.
APPLICANT: McLaughlin, Megan M.
APPLICANT: Torphy, Theodore J.
TITLE OF INVENTION: Human Brain Phosphodiesterase
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Patents/ P.O.Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,521B
FILING DATE: October 2, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,386
FILING DATE: 22 May 1995
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,334
FILING DATE: 10 March 1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth J. Hecht
REGISTRATION NUMBER: 41,824
REFERENCE/DOCKET NUMBER: P50145C1FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5009
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-942-521B-8

Query Match 24.5%; Score 550; DB 2; Length 562;
Best Local Similarity 31.8%; Pred. No. 4.5e-50;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

QY 8 RMLGDRVRVRAGFESERRGSHPIYDPRIFHSQSEIEVSVSARNIR-----LLSF 58
DB 82 RELTHLSEMSRSGNVSEYISNTFLD-----KQNDVEIPSPQDKREKKKKQQLMTQISG 136
QY 59 QRYLRSRFRFGTAVSN-SLNILDDYNGQAKCMLEKVGNNWDFILFDRLTNGNSLVSL 117
DB 137 VKLHMSSLNNTSISRGVNTENEDHLAKE---LEDLNKGLNIFNVAGYSHNRPLTCI 193
QY 118 TFLHLSLGLIEYFHLDMKRLRFLVMIQEDYHSONPYHNAVHAADVTQAMHCYKPEKL 177
DB 194 MYAIFQERDLKTKFISDFTVYMTLEHDYHSDVAYHNSLHAADVAQSTHLLSTPAL 253
QY 178 ANSVTPWDILLSLAAATHDLHPGVNQPFLIKTNHYLATLYKNTSVLENHHWSAVGLL 237
DB 254 DAVFTDLEILAAIFAAAHVDHPGVSNQFLINTNSLALMYNDESLENHHLAVGFKLL 313
QY 238 RES--GLFSLHPLESRQOMETQIGALILATDISRQNEYSLSFRSHLD-----RGDLCL 289
DB 314 QEEHCDIFQNLTKKQRTLRKVIDMVLATDMSKMSLLADLKTMTVETKVTSSGVLLLD 373
QY 290 DTRRHVLVQALMKACADICNCRTWELSKOWSEKVTBEFFHQDIEKKYHILGVSPICDRH 349
DB 374 NYTDRIQVLRNMVHCADLSNPTKSLEYLRQWTDRIEMBEFFQOGDKERERGMEISPMCDKH 433
QY 350 TESTANTQIGFTYVLEPLFTEWA 373
DB 434 TASVEKSGVGFIDYVHPLMETWA 457

RESULT 11
US-08-474-379C-4
Sequence 4, Application US/08474379C
Patent No. 5977305
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/474,379C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/206,188
; FILING DATE: 01-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,352
; FILING DATE: 19-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 27866/32771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-379C-4

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Query Match 24.5%; Score 550; DB 2; Length 562;
Best Local Similarity 31.8%; Pred. No. 4.5e-50;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

Qy	8	RMLGDVVRGRAGPESRRSGHPYIDPRIFHSQSEIEVSVARNRR-----LLSF	58
Db	82	RELTHLSEMSGVSGVSEYISNTFLD-----KQNDVIPPTQXDRBKKKKQLMTQIS	136
Qy	59	QRYLRSRFRFGTAVSN-SNLILDDYNGQAKMLEKVGWNWDFLFDRLTNGNSLAVSL	117
Db	137	VKJMHSSLNNTSISRFQVNTNEDHLAKE---LEDLNKGLNIFNVAGVSHNRPUTCI	195
Qy	118	TFHLFSLHGLTIEYFHLDMVKLERFLVMIQBDYHSQNPYHNAVAADVTQAMHCYLKEPKL	177
Db	194	MYAIFQERDULLTKFKISSDTPVTYMTLEHDHYHSDVAYHNSLHAADVAQSTHVLSTPAL	253
Qy	178	ANSVTPDWILLSLIAATHDLHGVSQNPFLIKTNHYLATLYKNTSVLENHWHRSVGLLL	237
Db	254	DAVFDTLEILAAIPAAATHVDHPGVSNQFLINTNSELALMYNDESVLNHHLVAFGFKLL	313
Qy	238	RES--GFSLHPLSRQOMETQIGALITLADTISRQNEYLSLFRSHLD-----RGDLCLE	289
Db	314	QEEHCDIFQNTTKQOROTLRKOWIDMVLATDMKMSLLADLTKMTVETKTKVTSSGVLLLD	373
Qy	290	DTRHRHVLQWALCKADICNPRCTWELSKOWSEKVTEEFFHQGDIEKKYHLGVSPCLDRH	349
Db	374	NYTDRIQVLRNMVHCADLSNPTKSLEYLRQWTDRIIMEEFFQGDKERERGMSEI5PMCDKH	433
Qy	350	TESTANIQIGFMTYVLVBPLFTFWA	373
Db	434	TASVEKSVQGFIDYIVHPLMETWA	457

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RESULT 12
US-09-146-249A-4
; Sequence 4, Application US/09146249A
; Patent No. 6069240
; GENERAL INFORMATION:
; APPLICANT: Wigter, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
;

```

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,249A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-146-249A-4

Query Match 24.5%; Score 550; DB 3; Length 562;
Best Local Similarity 31.8%; Pred. No. 4.5e-50;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

[illegible]

RESULT 13
US-08-206-188B-4
; Sequence 4, Application US/09206188B
; Patent No. 6100025
; GENERAL INFORMATION:
; APPLICANT: Wigter, Michael H.
; APPLICANT: Colicelli, John J.

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; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,188B
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36107
; TELEPHONE: 312/474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-206-188B-4
```

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Query Match      24.5%; Score 550; DB 3; Length 562;
Best Local Similarity 31.8%; Pred. No. 4.5e-50;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

Qy      8 RMLGDVVRVRAGFESRGRGSHYIDFRIFHSQSEIEVSVSARNIR-----LLSF 58
Db      82 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPQDKREKKKQQLMTQISG 136
Qy      59 QRYLRSRFRFGTAVSN-SLNIILDDYNGQAKCMLEKVGNNFDFLFDRLTNGNSLYSL 117
Db      137 VKLHSSSLNNTSISRFVNTENEDHLAKE---LEDLNKGLNIFNVAGYSHNRPLTCI 193
Qy      118 TFLHLSLGLIEYFHLDMKMLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
Db      194 MYAIFQERDLKTKFKISSDTFTVYMTLEDHYHSDVAYHNSLHAADVAQSTHVLSTPAL 253
Qy      238 RES--GLFSLHPLERQOMETOIGALIIATDISRQNEVLSLFRSHLD-----RGDLCL 289
Db      314 QEEHCDIFQNLTKKQRTLRKQVDMVLATDMKMSLLADLKTWVTKKVTSSGVLLLD 373
Qy      290 DTRHRLHYLMALKACADICNPCRTEWLSQKWEKTEEFPHQGDIEKHYHGVSPCLDRH 349
Db      374 NYTDRIQVLRNMVHCADLSNPKTSLEYLRQWTDRIWEFFQQGDKERERGMESPMCDKH 433
Qy      350 TESIANIQIGFWTYLVEPLFTWA 373
Db      434 TASVEKSVQGFIDYIVHPLWETWA 457
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RESULT 14

PCT-US91-02714-4

; Sequence 4, Application PC/TUS9102714

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; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02714
; FILING DATE: 19910419
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 27805/30197
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US91-02714-4

Query Match      24.5%; Score 550; DB 5; Length 562;
Best Local Similarity 31.8%; Pred. No. 4.5e-50;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

Qy      8 RMLGDVVRVRAGFESRGRGSHYIDFRIFHSQSEIEVSVSARNIR-----LLSF 58
Db      82 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPQDKREKKKQQLMTQISG 136
Qy      59 QRYLRSRFRFGTAVSN-SLNIILDDYNGQAKCMLEKVGNNFDFLFDRLTNGNSLYSL 117
Db      137 VKLHSSSLNNTSISRFVNTENEDHLAKE---LEDLNKGLNIFNVAGYSHNRPLTCI 193
Qy      118 TFLHLSLGLIEYFHLDMKMLRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
Db      194 MYAIFQERDLKTKFKISSDTFTVYMTLEDHYHSDVAYHNSLHAADVAQSTHVLSTPAL 253
Qy      178 ANSVTPDWILLSLAAATHLDHGVNQPFLLKTNHYLATLYKNTSVLENHHWRSVAGLL 237
Db      254 DAVFTDLEILAAIAFAAAHVDHPGVSNQFLINTNSALMYNDSVLENHHLAVGFKLL 313
Qy      238 RES--GLFSLHPLERQOMETOIGALIIATDISRQNEVLSLFRSHLD-----RGDLCL 289
Db      314 QEEHCDIFQNLTKKQRTLRKQVDMVLATDMKMSLLADLKTWVTKKVTSSGVLLLD 373
Qy      290 DTRHRLHYLMALKACADICNPCRTEWLSQKWEKTEEFPHQGDIEKHYHGVSPCLDRH 349
Db      374 NYTDRIQVLRNMVHCADLSNPKTSLEYLRQWTDRIWEFFQQGDKERERGMESPMCDKH 433
Qy      350 TESIANIQIGFWTYLVEPLFTWA 373
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Db 434 TASVEKSVQGFIDYIVHPLWETWA 457

RESULT 15

US-08-942-521B-2
; Sequence 2, Application US/08942521B
; Patent No. 5932477
; GENERAL INFORMATION:
; APPLICANT: Livi, George P.
; APPLICANT: McLaughlin, Megan M.
; APPLICANT: Torphy, Theodore J.
; TITLE OF INVENTION: Human Brain Phosphodiesterase
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SmithKline Beecham Corporation
; STREET: Corporate Patents/ P.O.Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/942,521B
; FILING DATE: October 2, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,334
; FILING DATE: 10 March 1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth J. Hecht
; REGISTRATION NUMBER: 41,824
; REFERENCE/DOCKET NUMBER: P50145C1FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5009
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 564 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-942-521B-2

Query Match 24.5%; Score 550; DB 2; Length 564;
Best Local Similarity 31.8%; Pred. No. 4.6e-50;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;
QY 8 RMLGDVRSRAGFESRGRGSHPIYDFRPHSQSEIEVSVSARNRR-----LLSF 58
Db 84 RELTHLSERSRSGNQSVYISNTFLD-----KQNDVEIPTSPTQDKREKKKQQLMTQISG 138
QY 59 QRYLSRSRFRGPAVN-SLNILDDYNGQAKCMLEKVGWNPFDFLRLTNGNSLVL 117
Db 139 VKKLHSSSLNNTSISRFQVNTENEDHLAKE---LEDLAKWGLNIFNVAGYSHNRPLTICI 195
QY 118 TFLHLSHGLIEVHFLDMKRLRFLVMIQEDYHSQNPYHNAVHAAVDTQAMHCYLKEPKL 177
Db 196 MYAIFOERDLKTFRISSDFTIYMTLTEDHYHSDVAYHNSLHAADVQSTHVLSTPAL 255
QY 178 ANSVTPWDILLSIAAATHDLDPGVNOPELITNHYLATLYKNTSVLENHWRSAVGLL 237
Db 256 DAVFTDLLEILAAIFAAAIHVDHFGVSNQFLINTNSLALMYNDESVLNHLAVGFKLL 315
QY 238 RES--GLFSLPLESRQOMETQIGALILATDISRQNEYSLSFRSHLD-----RGDLCL 289

Db 316 QEEHCDFPMNLTKQROTLRKQVIMVLDVLTADMSKMSLLADLKTWVETKKTSSGVLILD 375
QY 290 DTRHRHVLQALKCADICNPCRTHWELSKQWSEKYTEEFFHOGDIEKKYHLGVSPICDEH 349
Db 376 NYTDRIQVLRNVMVHCADLSNPTKSLLEYRQWTDRIIMEEFFQOGDKERBERGMEISPMCDKH 435
QY 350 TESIANIQIGFWTYLVEPLFTWA 373
Db 436 TASVEKSVQGFIDYIVHPLWETWA 459

Search completed: May 26, 2004, 09:29:02
Job time : 24 secs

!!AA MULTIPLE ALIGNMENT 1.0
PileUp of: us*

Symbol comparison table: GenRunData:blosu62.cmp CompCheck: 1102

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GapLengthWeight: 2

align123.msf MSF: 426 Type: P May 28, 2004 08:13 Check: 4342 ..

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us-09-966-781a-3		RQMEQAQIGA	LILATDISRQ	NEVLSLFRSH	LDKGDHLDD	GRHRLVLQM	
us-09-966-781a-1		RQMETQIGA	LILATDISRQ	NEVLSLFRSH	LDKGDLCLED	TRHRLVLQM	
us-09-966-781a-2	301	ALKCADICNP	CRNWELSKQW	SEKVTBEFFH	QGDIEKKYHL	GVSPCLDRQT	350
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us-09-966-781a-2	401	QPPSSSDANA	AFELNSQLIT	QENRLS			426
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